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Regult
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2 6/prodata/1.

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5: /cgn2 6/prodata/1.

6: /cgn2 6/prodata/1.
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/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptodata/1/iaa/backfiles1.pep:*
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sequence 5278, Applisequence 2, Applisequence 7, Applisequence 16, Applisequence 16, Applisequence 16, Applisequence 16, Applisequence 16, Applisequence 2, Applisequence 3, Applisequence 4, App
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5278, Ap
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RESULT 2  SEQ=114-001C-5278  SEQ=114-001C-5278  SEQ=114-001C-5278  PATION NO. 5360700  CENERAL INFORMATION: APPLICANT: Lynn Doucetre-Stamm et al TITLE OF INVENTION: AUCUEIC ACID AND ANIXO ACID SEQUENCES RELATING TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS FILLE REFERENCE: GTC.07  CURRENT PAPLICATION NUMBER: US/09/134,001C  CURRENT PAPLICATION NUMBER: US 60/064,964  DRIGE STITLED ANDE: 1398-06-13  DRIGE STITLED ANDE: 1398-06-13  DRIGE STITLED ANDE: US 60/064,964	Query Match 100.0%; Score 86; DB 4; Length 33: Best Local Similarity 100.0%; Pred. No. 9.5e-07; Matches 15; Conservative 0; Mismatches 0; Indels 27 27 28 29 20 21 WYMERRNLEEDDYL 15 21	CURRENT APPLICATION NUMBER: US/09/322.873A CURRENT FILMS DATE: 1999-60-10 PRIOR FILMS DATE: 1999-60-10 PRIOR PELING DATE: 1999-60-10 PRIOR PELING DATE: 1998-06-01 PRIOR PELING DATE: 1998-06-03 PRIOR FILMS DATE: 1998-06-30 PRIOR FILMS DATE: 1998-06-30 SOFTWARE: PAST SEQ for Windows Version 4.0 SEQ ID NO 2 SEQ ID NO 2 SEQ ID NO 2 SEQ ID NO 3	NSMEMBRANE ANTIGE	ALIGNMENTS	28 36 41.9 20.2 3US-08-980-557-6 29 36 41.9 373 4 US-09-153-161.3 36 41.9 437 4 US-09-134-001C-3418 Sec. 31 36 41.9 447 3 US-09-134-001C-5673 32 36 41.9 449 4 US-09-134-001C-5673 33 36 41.9 550 1 US-08-484-434-2 34 41.9 550 1 US-08-484-434-2 35 36 41.9 550 1 US-08-49-124-2 36 41.9 550 1 US-08-49-124-2 36 41.9 550 4 US-09-149-914-4 36 41.9 1854 4 US-09-149-913-2 36 41.9 1854 4 US-09-149-913-2 37 4 41.9 1854 4 US-09-149-108 38 41.9 2291 2 US-08-819A-29 39 36 41.9 2291 2 US-08-819A-29 39 36 41.9 2291 2 US-08-980-357-29 39 36 41.9 2291 3 US-08-980-537-29 39 31.3 41.3 273 4 US-09-650-685-7 39 31.3 41.3 273 4 US-09-650-685-7 39 31.3 41.3 273 4 US-09-650-685-7 39 35 41.3 273 4 US-09-650-6840-2 39 35 41.3 273 4 US-09-651-685-7 39 36 41.9 2891 4 US-09-651-685-7 39 38 41.9 2891 4 US-09-651-685-7 39 39 39 39 39 39 39 39 39 39 39 39 39 3
검	9; 0; Gaps		NS		sequence 6, Appli sequence 318, Appli sequence 317, Appli sequence 567, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 2, Appli sequence 4, Appli sequence 2, Appli sequence 29, Appli sequence 29, Appli sequence 29, Appli sequence 29, Appli sequence 7, Appli sequence 7, Appli sequence 7, Appli sequence 7, Appli sequence 7, Appli sequence 7, Appli
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rococcus

PRIOR FILING DATE: 1997-11-08

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GENERAL INFORMATION:
APPLICANT: MOGONIGLE, BRIAN
APPLICANT: MOGONIGLE, DANIEL
TITLE OF INFERTION: SOFBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: CL-1108-A
FILE REFERENCE: CL-1108-A
CUURENT APPLICATION UNMER: US/09/247,373B
CUURENT FILING DATE: 1997-02-10
PRIOR FILING DATE: 1997-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 56
LENGTH: 221
TIPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08403866 Patent No. 5643779 GENERAL INFORMATION:
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Best Local
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PRIOR FILING BATE: 1997-08-14
NUMBER OF SEG ID NOS: 5674
SEG ID NO 5278
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CAPPLICANT: F
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                                                                                                                                                                  NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Fatentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                 ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, Michael L.
REGISTRATION NUMBER: 30, 727
REFERENCE/DOCKET NUMBER: 207.
                                                                                                                                                                                                                                                                                                                   APPLICANT: Ehrlich, Stanislav
APPLICANT: Ehrlich, Stanislav
APPLICANT: Renault, Plerre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: Synthase from Lactococcus and its applications
TELECOMMUNICATION INFORMATION:
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                                                                                              APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 435
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Local Similarity 44.4%; Pred. No. 2
168 8; Conservative 3; Mismatch
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Local Similarity 64.3%;
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Pred. No. 12
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Query Match
Best Local Similarity
Matches 7; Conserve
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US-08-651-999A-7
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  Best Loc
Matches
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                                Query Match
                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA.

APPLICATION NUMBER: US/08/651,999A
FILING DATE: MAY 23, 1996
ATTORREY/AGENT IMPORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE DOCKET NUMBER: 6700/395
TELECOMMUNICATION IMPORMATION:
TELECOMMUNICATION IMPORMATION:
                                                                                                                                                                                                         TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM;
MEDIUM TYPE: J.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
ORGANISM: Lac
                                                                                                                                                                           SEQUENCE CHARACTERISTICS
LENGTH: 968 amino acid
                                                                                              MOLECULE TYPE:
DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Stefan Somlo and Toshio Mochizuki
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
TITLE OF INVENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: pi
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TYPE: amino acid
TOPOLOGY: 14-
Local Similarity
les 6; Conserv
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STATE: NEW YORK
                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                          TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                 TOPOLOGY:
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                                                                                                                                                         : 968 amino acids
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978450 (WUT)
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                                                                              no NO
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                   46.2%;
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Pred. No.
  Score 38; DB 3;
Pred. No. 2.9e+02;
2; Mismatches 5
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                                Length 968;
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GENERAL INFORMATION:
APPLICANT: Stefan
                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08061376
Patent No. 6175000
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 697-5995
TELEPAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-591-4766
TELEX: TWX 75-591-4766
TRORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPA:
OPERATING SYSTEM: MS-DO
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
                     APPLICANT: EVAIB, Glen A.
APPLICANT: DJADAIL, MALEK
APPLICANT: SELLET, MALEK
APPLICANT: SELLET, MICHA
APPLICANT: SELLET, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 968 amino acid
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APPLICATION NUMBER: 08/651,999
FILING DATE: WAY 23, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stefan Somlo and Toshio Mochizuki
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
TITLE OF INVENTION: AND USES THERBOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 WKMQPSNQTEADN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/385,752 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WKMKPRRNLEEDD 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 2.9e+02;
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Best Local Similarity 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/08468709B
           APPLICATION NUMBER: US/08/468,709B
FILING DATE: 06/06/95
CLASSIFICATION: 43
ATTORNEY/ACENT INFORMATION:
NAME: Smith, Deann F.
REGISTRATION NUMBER: 36.603
REFERRENCE/DOCKET NUMBER: 6.613
REFERRENCE/DOCKET NUMBER: 7115-00676DVF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION INVERSE: 31,192
REGISTRATION INVERSE: 11,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                             COMPUTER READABLE FORM,
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tavakkol, Amir
TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Astrom, Anders
APPLICANT: Voorhees, John
APPLICANT: Pattersson, Ulrika
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424 PRRFIEDEDY 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0
FILING DATE: 13-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 48303
                                                                                                                                                                                                                                                                                                                                                                      CITY: Bloomfield Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: unknown
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TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                               Michigan
                                                                                                                                                                                                                                                                                                                                                                                       E: Harness, Dickey & Pierce, P.L.C.
PO Box 828
                                                                                                                                                                                                                                                                                                                              United States of America
(810) 641-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.2%;
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Pred. No. 1.4e+03;
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US-08-969-106-4
                              RESULT 10
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; MOLECULE TYPE: peptide
US-08-241-664B-16
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                                                                                                                                                                                                                                                                              Query Match 43.0%; Score 37; DB 2; Best Local Similarity 54.5%; Pred. No. 7.9; Matches 6; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIDIN TYPE: Floppy disk
COMPTIER: IMP NC Compatible
OPERATING SYSTEM: P-DOS/MS-DOS
SOFTWARE: PACENTIN E-DOS/MS-DOS
SOFTWARE: PACENTIN E-Lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/241,664B
FILING DATE: May 11, 1994
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TELEX: 287637
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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LENGTH: 25 amino acids
TYPE: amino acid
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APPLICANT: Astrom, Anders
APPLICANT: Patterseon, Ulrika
APPLICANT: Tavakkol, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: HUMAN CRABP-I AND CRABP-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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Local Similarity 54.5%;
hes 6; Conservative
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TYPE: amino acid
TOPOLOGY: unknown
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                                                                                                                                                                                                             1 WKMKPRRNLEE 11
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                                                                                                                                       WKMRSSENFEE 17
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: United States of America
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PO Box 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (810) 641-0270
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Pred. No.

    Mismatches

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                                                                                                                                                                                                                                                                                                                                                         Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08252995D Patent No. 5650501
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Patent No. 5986055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.0%; Score 37; DB 2; Best Local Similarity 50.0%; Pred. No. 1.3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IRM Compatible
OREATING SYSTEM, DOS
SOFTWARE: FRACESD VARIOUS 2.0
CURRENT APPLICATION HOMESR: US/08/969,11
FILING DATE: 13-MOV-1597
FILING DATE: 13-MOV-1597
FILING DATE: 13-MOV-1597
ATTOMNET/AGENT IMPORMATIO:
NAME: MESTOCK, S. Lesite
NAME: MESTOCK, S. Lesite
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
COUNTRY: Canada
ZIE: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PREDELIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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APPLICANT: Schulz, V.
TITLE OF INVENTION: CDK2 INTERACTIONS
                                                                                                                                                                                                                                                                                                           APPLICANT: Dennis, Jam
APPLICANT: Heffernan,
APPLICANT: Fode, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 KKRKGYEDDDYV 303
                                                                                                                                                                                    STREET: 40 King Street West
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                Ontario
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                               Heffernan, Mike
                                                                                                                                                                                                                                                                                                                                                  Dennis, James W
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US-08-834-108-2
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                                                                                                                             TELEPHONE: (416) 364-7311
TELEPAX: (416) 361-1399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 416 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOS: linear
                                Matches
                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Applic
Patent No. 5976893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                               CLASSIPICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: KUTÓYÓY, LÍNĜA M
REGISTRATION NUMBER: 31,971
REFERENCY_DOCKET NUMBER: 31,971
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 364-73
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Dennis, James W
APPLICANT: Heffernan, Mike
APPLICANT: Fode, Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                               MOLECULE TYPE: protein
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Local Similarity 54.5%;
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 02-JUN-1994
CLASSIFICATION: 536
                              Local Similarity
mes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Can
ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 416 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 3153-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kurdydyk, Linda M
REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
4 KPRRNLEEDDY 14
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                                              43.0%;
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Pred. No.
                                                                                                                                                                                                                                                                 3153-210
                                              Score 37;
Pred. No.
                                              DB 2; I
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                                1; Indels
                                                              Length 416;
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RESULT 13
US-08-252-995D-6
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                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08834108 Patent No. 5976893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.0%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (416) 364-73
TELEPAX: (416) 361-1398
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-UM-1994
CLASSIFICATION: 316
ATTOONINY/AGENT INFORMATION:
NAME: NUA-1994/H, LIICH M
REGISTRATION WINBER: 31, 971
REFERENCE/JOCKET NUMBER: 3115
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                  APPLICANT: Dennis, James W
APPLICANT: Referran, Mike
APPLICANT: Rode, Carol
TITLE OF INVENTION: NOVEL SERINE/THREONINE KINASE
NUMBER OF SEQUENCES: 14
AUDRESSE: BERESKIN 4 PARR
AUDRESSE: BERESKIN 4 PARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||:|:|: :
406 KPRRSLDENQH 416
                                                                               STREET: 40 Kin
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                      406 KPRRSLDENOH 416
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 464 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      STATE: Ontario
COUNTRY: Canada
ZIP: M5H 3Y2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 KPRRNLEEDDY 14
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                                                                                                                  40 King Street West
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOVEL SERINE/THREONINE KINASE
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Pred. No. 1.9e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 464;
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CLASSIFICATION. 536
ATTOME! AUTOMIC INFORMATION:
NAME: KNIDYDY, Linda M
RESISTRATION UNMER: 34.971
REFERENCE/DOCKET NUMBER: 353
TELECHONE: (446) 364-731N:
TELEPHONE: (446) 364-731N:
TELEPHONE: (446) 361-398
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acide
TYPE: mino acid
TOPOLOGY: linear
MOLECULE TYPE: procein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-484-105-24
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BELL, Stephen by APPLICANT: KOBAKYASHI, Rydi APPLICANT: KOBAKYASHI, Rydi APPLICANT: ROBENTASHI, Rydi APPLICANT: ROSS, MARSHI, PARTICLE APPLICANT: LAURENSON, PARTICLE APPLICANT: LAURENSON, PARTICLE APPLICANT: LI, JOSACHIM JAPPLICANT: GAVIN, KIMDERIJ OF REBILICATION COMPLEX GENES NUMBER OF SEQUENCES: 24

APPLICANT: GAVIN, KIMDERIJ OF REPLICATION COMPLEX GENES NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS: 12

ADDRESSES: PLERR, HOHBACH, TEST, ALBRITTON & HERBERT STATE: CALIFORNIAGO CONTRET: USA COUNTRY: USA 2IP: 94111-4187

COMPUTER READABLE FORM: MEDIA COMPUTER READABLE FORM: POPUS MS-DOS OPTWARE: PAPPLICATION DATA: DOS OPTWARE: PAPPLICATION DATA: DOS DETWARE: PAPPLICATION DATA: DAPPLICATION MATA: LABRITON HIBS DOS DAPPLICATION MATA: LABRITON HIBS DESCRIPTION MATA: LABRITON MATA: LABR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 43.0%; Score 37; DB 2; Best Local Similarity 54.5%; Pred. No. 1.9e+02; Matches 6; Conservative 4; Mismatches 1
                                                          APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT IMPORMATION:
ANAME: COMMAN Ph. D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,932/DJB/RAO
TELECOMMUNICATION IMPORMATION:
TELEROME: (415) 494-8700
TELEROME: (415) 494-8700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5589341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24,
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,108
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        406 KPRRSLDENQH 416
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Search completed: March 26, 2003, 16:51:37 Job time : 11.593 secs
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                                                                                                            Best Local Similarity
Matches 7; Conserv
                                                                                                              Matches
                                                                                                                                       Query Match
                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                            LENGTH: 577 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                         52 KPEYDLEEDD 61
                                                                                   4 KPRRNLEEDD 13
                                                                                                              Conservative
                                                                                                                         70.0%;
                                                                                                              1;
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Database
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Listing first 45 summaries
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1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen_Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

SUMMARIES	

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ABB95387	ABG61813	AAM01282	AAM78845	AAU69927	AAY58194	AAY12304	AAY12305	AAE02784	AAY58201	DB ID
Human P789P protei	Prostate cancer-as	P789P amino acid s	Human protein SEQ	Human prostate cDN	Human STRAP-1 prot	Human 5' EST secre	Human 5' EST secre	Immunogenic peptid	Human STRAP-1 pept	Description

400	4 4 6 0 0	4 4 4	441	22	41	41.5	4.2 4.2	4 4 2 2	4 4	2 2 2	42.5	4 4 3 v	45	45	70	96	86
999	46. 55. 55.		677		47.7 47.7	48.8 48.3	48.8 8.8	48.8		. 00 .		50.0			81.4 71.4	0	100.0
236 257 258	223 224 224	197 205 221	738	271 327	166 192	1417 208	1019	959	165	164	256	2040	421	72	95 r	375	374
23 23	212	21 21	222	21 22	21 21	222	23 22	22	22	22	3 23	23	22	22	200	22	22
ABP29691 ABP30273 ABP25968	AAB62225 AAG24829 AAG39745	AAW98006 AAG38584 AAB07850	ABB65092 ABB65092 AAU01103	AAG30005 AAM40194	AAG30007 AAG30006	ABB63329 AAU18520	AAU75900 AAU07892	AAU03543 AAU07874	AAG67877	AAB35757	ABP40433	ABB04597	ABG25522	ABG25517	AAY11840	AAE02780	AAM79829
C C C	Glycine max glutat Arabidopsis thalia Arabidopsis thalia	Human interleukin- Arabidopsis thalia Amino acid sequenc	Drosophila melanog Gene 41 Human secr	dopsis polype	Arabidopsis thalia Arabidopsis thalia			Polypeptide sequen	Equine infectious	e:	Staphylococcus epi	Lettuce big-vein v	human	human di	Human 5' EST secre	six tra	Human protein SEQ

# ALIGNMENTS

AAY58201 standard; peptide; 15 AA.

AAY58201;

14-MAR-2000 (first entry)

Human STRAP-1 peptide 1, corresponding to STRAP-1 residues 14-28.

transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunisation; immune response; drug targetting; recombinant protein cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; prognosis; monitoring; susceptibility; therapeutic inhibitor;

Synthetic. Homo sapiens

W09962941-A2

09-DEC-1999

RESULT 1
AAYSS201
AAY 01-JUN-1998; 30-JUN-1998; 01-JUN-1999; 98US-0087520. 98US-0091183. 99WO-US12157

(UROG-) UROGENESYS INC. (AFAR/) AFAR D E. (HUBE/) HUBERT R S.

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RESULT 2
AAE02784
ZEXEXEX
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                                                                                                                                                                                                                                                                                                                                                                              the producte, Anytonic share, twenputchile transmembrate antigenous the projectional anti-STRAP-1 N-terminus antibodies in sheep. The call instance were used to probe western blots of cell lysates from the antibodies were used to probe western blots of cell lysates from the prostate and non-prostate cancer cell lines, and in immunchistochemical analysis of STRAP-1 expression. STRAP-1 is the prototype cannot be strated and non-prostate cancer cell lines, and in immunchistochemical cannot be supposed to the strate the structural conservation, but which show the structural to the strate of the strate prototype calls in normal human tissues. Structurally, STRAP-1 is thought to be a type life membrane protein and is expressed predominantly in prostate and the strate protein characterised by six transmembrane domains and to intracellular N and C-termini, suggesting that it folds in a "serpentine" manner into three extracellular and two intracellular loops. STRAP-1 manner into three extracellular and two intracellular loops. STRAP-1 manner into three extracellular and two intracellular loops. STRAP-1 manner into three extracellular and two intracellular loops. STRAP-1 manner into three extracellular and two intracellular loops. CTRAP-1 manner into three extracellular and two intracellular loops. STRAP-1 manner into the strate of the STRAP protein is not known. They may be iden charged by certain into charges in not known. They may be used for detection, prognosis, and monitoring of cancers (or susceptibility to cancer), as therapeutic coinfibitions of to target therapeutic sendence in thibitors of strap expression and for therapeutic coinfibitions of strap expression and for therapeutic coinfibitions of strap expression and for therapeutic coinfibitions are expressed on the scall surface, they are expressed mainly of protein and the effects on other tissues.
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Best Local &
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a synthetic peptide (peptide 1) corresponding to residues 14 28 of STRAP-1 (serpentine transmembrane antigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-072832/06.
               Immunogenic
                                                       06-AUG-2001
                                                                                            AAE02784;
                                                                                                                              AAE02784 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                  1 WKMKPRRNLEEDDYL 15
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) RAITANO A B.
) SAFFRAN D C.
                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                 15 AA;
               peptide #1 of human STEAP-1
                                                                                                                                                                                                                                                                                                       Conservative
                                                    (first entry)
                                                                                                                                                                                                                                                                                                  100.0%; S-
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2000; 2000WO-US33040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3C; Page 77; 187pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New STEAP (six transmembrane proteins, expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-367804/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jakobovits A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hubert RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0455486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raitano AB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epithelial antigen of the prostate) cancers, useful for detecting and treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Faris M;
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The present invention relates to human six transmembrane spithelial surface serpentine transmembrane antigens. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP gene is used in gene therapy. Inhibiting the development or progression of a cancer (eg. transmembrane antigens) and paceratic expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient. Treating to comprises administering a vaccine composition to the patient. Treating capture in a patient with a cancer that expresses STEAP or inhibiting growth or killing cells expressing STEAP, comprises administering to the patient at vector encoding single chain monoclonal antibody that comprises the vector encoding single chain monoclonal antibody that comprises the transmission of the heavy and light chains of the monoclonal antibody that comprises the single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody coding sequence to the cancer cells and the encoded single chain monoclonal antibody is expressed.

Comprises the present sequence is an immunogenic peptide of STEAP-1. STEAP-1 gene is located on chromosome 7p2.3. This peptide is used to immunise sheep for the generation of sheep polyclonal antibodies towards the amino-terminus of anti-STEAP-1.

Sequence 15 AA;

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                                 Matches
                                                  Query Match
                                          Local Similarity
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               1 WKMKPRRNLEEDDYL 15
 WKMKPRRNLEEDDYL 15
                                  15;
                                 100.0%;
ilarity 100.0%;
Conservative 0
                                  0
                                          Score 86;
Pred. No.
                                   Mismatches
                                 4.6e-08;
hes 0;
                                                   DB 22;
                                                   Length 15;
                                  0,
                                  Gaps
                                   0
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RESULT 3
AAY12305
ID AAY1
AAY12305
                    AAY12305 standard; Protein; 66
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Human 5'
                          17-JUN-1999
                          (first entry
 secreted protein
 SEQ ID NO: 336
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22222XBXBXXX Human; secreted protein; EST; expressed sequence teg, diagnosis; foresisi; gene therapy, chromosome mapping; signal peptide; objected therapy, cytokine activity, real proliferation; differentiation; haematoppissis regulation; tissue growth regulation; reproductive hormone regulation; chemocactic; chemokinetic; haemostatic;

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RESULT 4
ANY12304
ID AAY1
IX XX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins obtained may have cytokine activity, cell proliferation/differentiation activity, tiesue growth regulating activity, reproductive hormone regulating activity, these sectivity, chemokantic activity, has measure and thrombolytic activity, respectivity (other shratic activity, has measure and thrombolytic activity, receptor/ligand activity, anti-filammatory activity, recursivity, receptor/ligand activity, anti-filammatory activity, recursivity or activity anti-filammatory activity. In the second of the recursive filament of the sequence on also be used for abcalling corresponding promoter as equence. The mental actide encoding the signal peptide can be used for directing extracellilar secretion of a polypeptide or the insertion of a polypeptide into a cell.
                                                                             Human, secreted protein, EST, expressed sequence teg, diagnosis, forensis; gene therapy, chromosome mapping; signal peptide; upstream regulatory sequence; cyrokine activity, cell proliferation; differentiation, haematopoissis regulation; tissue growth regulation; reproductive hormore regulation; chemocactic; chemokinetic; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human secreted proteins, and encode the proteins given in AXY12281 to AXY12514, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The muleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for disposis and therapy. The
                                                                                                                                                                                                             Human 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAX12261 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; Page 677-678; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acide encoding human secreted proteins - obtained from CDNA libraries prepared from e.g. liver, overy, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  thrombolytic; anti-inflammatory; tumour inhibition.
                                                              thrombolytic;
                                                                                                                                                                                                                                                                                                                                             AAY12304 standard; Protein; 109 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 WKMKPRRNLBEDDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
wes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WKMKPRRNLEEDDYL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-153778/13
                                                                                                                                                                                                             EST secreted protein SEQ ID NO:335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                          (first entry)
                                                              anti-inflammatory; tumour inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0905135
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Pred. No.
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Best Local
                                                                                                                                                                                                                                                                                                      Human STRAP-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                          AAY58194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1997;
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                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proteins obtained may have cytokine activity, cell proteins obtained may have cytokine activity, cell productive hormone activity, tissue growth regulating activity, responderive hormone regulating activity, chemotactic Activity, themostatic and thrombolytic activity, receptor! Igand activity, self-lammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences of the mucleic acids encoding the signal peptide can be used for directing extracellular secretion of a gipal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a directing extracellular secretion of a polypeptide or the insertion of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding human secreted proteins - obtained from cONA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human secreted proteins, and encode the proteins given in AY12261
AY12514, respectively. The proteins given represent the signal year
and an N-terminal fragment of a secreted protein. The nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; Page 677; 824pp; English.
                                                                                                 polypeptide into a membrane, or importing a polypeptide into a cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1999-153778/13.
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109 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0905135
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14 WKMKPRRNLEEDDYL 28
                   1 WKMKPRRNLEEDDYL 15
                                                     Similarity
                                          Conservative
                                                   100.0%;
                                          0
                                                   Score 86; DB 20;
Pred. No. 3.8e-07;
                                          Mismatches
                                                               Length 109;
                                          0
                                         Gaps
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AAYS8194 standard; Protein; 339 AA.

Key Region Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; prostate; prostate cancer; prostate cancer; bladder cancer; colon cancer; pancreatic cancer; ovarian cancer; tumour antigen; immunation; immuna response; cellular; humoral; anticancer vaccine; antibody, detection; diagnosis; cellular; humoral; asticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein Location/Qualifiers ۳,

/note= "Intracellular region

Homo sapiens

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Complia sequence expresents a novel human protein. STRAP-1 (serpentise curtansambrane autign of the proteins. STRAP-1 is the proteyne member of the STRAP family of proteins (ANSS194-YES197) which control is the protein strain of the proteins (ANSS194-YES197) which control is a strain of the protein strain of the protein strain of the protein strain of the strain o
gap-junction proteins (from immunohidrochemical staining) STRAP-1 and STRAP-2 are cell-surface tumour sattigens, immunisation with a STRAP protein induces callular and humoral immune responses againty STRAP proteins be used to identify specific-binding agents, to produce anticancer vaccines and to generate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             particularly for prostatic cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel proteins useful as diagnostic markers
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HUBERT R S.
LEONG K.
RAITANO A B.
SAFFRAN D C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1A; 83pp; English
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98US-0091183.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .63..184
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RESULT 6
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ID AAU69927
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12-MAY-2000; 2000US-0570737;

13-JUN-2000; 2000US-0593793;

27-JUN-2000; 2000US-0505783;

10-AUG-2000; 2000US-0505783;

10-AUG-2000; 2000US-0551236;

66-SEP-2000; 2000US-0571236;

66-SEP-2000; 2000US-0579426;
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                                                                                                                                                                                                                                                                                                                 WPI; 2001-639232/73.
N-PSDB; AAS64160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001; 2001WO-US09919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cDNA encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
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                                                                                                                                                                                                                           human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WKMKPRRNLEEDDYL 15
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                                                                                                                                                                                                                                                                                                                                                                                                   Dillon DC, Mitcham JL, Harlocker SL, Jiang GR, Retter MW, Stolk JA, Day CH, Vedvick Wang A, Skeiky YAW, Hepler WT, Henderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                   Harlocker SL, Jiang Y,
A, Day CH, Vedvick TS,
epler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalos MD;
Carter D;
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the

detecting the presence of

579pp; English.

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RESULT 7
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ID AAM7
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer, especially prostate cancer. The polypoptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypoptide are useful for stimulating an immune response, and for treating cancer. The oligomucleotide is useful for detecting cancer, The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                     Tang YT,
Zhao QA,
The invention relates to polymucleotides (AAS3145-AAS3415) and the encoded polymeptides (AAM3312-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides are useful in gene therapy, vaccines or peptide therapy. The polymeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haemacopolesis regulating e.g.
                                                                                                                                                                                                                                                        WPI; 2001-476283/51.
N-PSDB; AAK51978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; hammatopolesis; tissue growth factor; ammunomodujatory; cancer; leukeemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human
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                                                                                                                                                           Claim
                                                                                                                                                                                                 usetul
                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-SEP-2000;
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                                                                                                                                                                                                                                                                                                               Yang Y,
                                                                                                                                                                                               diagnosis and
                                                                                                                                                        Page 3800-3801; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nilarity 100.0%;
Conservative (
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2000US-0560875.
2000US-0598075.
2000US-0598075.
2000US-06520325.
2000US-0654936.
2000US-0653561.
2000US-0693325.
2000US-0728422.
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                                                                                                                                                                                                                                                                                                               Drmanac RT, Asundi V,
Wang J, Zhang J, Re
Wejhrman T, Goodrich
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Pred. No.
                                                                                                                                                                                               therapy
                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                     Zhou
                                                                                                                                                                                                                                                                                                                                       Chen
                                                                                                                                                                                                                                                                                                                                                             ۵,
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                                                                                                                                                                                                                                                                                                                       u C,
Wang
                                                                                                                                                                                                                                                                                                                                                          Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
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                                                                                                  The present invention describes polymuclectide sequences (I) which encode presente specific processes (II). (II) and (III) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II). (III) antibodies to (III). As in the specific processes comprising (II) and isolated (III) and insign processes comprising (III) and isolated (III) and itself to (III). The cancer that is a set of the section of cancer and partient. The cancer that III and (III) can be used in the detection of cancer that (II) and (III) can be used for monitoring the progression of cancer the antibodies or protecte cancer. (I) and (II) can be used for monitoring the progression of cancer the antibodies or local being the progression of cancer that all the progression continues when the sections of the sectio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosing, monitoring
for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment of cancer, leukaemia, nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 510-512; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2000; 2000US-0483672.
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                                                                          exemplification of
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MD, Fanger GR, Day
, Meagher MJ;
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                                                                          the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oding a prostate-specific protein, and treating prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ή̈́E
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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the sequence
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L, Skeiky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              patient
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Query Match

DB 22;

Length 339;

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RESULT 9
ABG61813
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                                      cancer-associated transcript in a cell from a patient. The method comprises contacting a biological semple from the patient with properties contecting a biological semple from the patient with the properties cancer-associated polymuclaorides (designated polymuclaorides (designated polymuclaorides designated and accordance associated polymuclaorides of various corganisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for disgnosing and tracting prostate cancer-associated genes are useful for disgnosing or treating prostate cancer-associated genes are identifying modulators of prostate cancer as well as for identifying modulators of prostate cancer are particularly useful in gene thereby, as a vaccine or in antisense applications.
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                                                                                                                                                                                                                                                                                                                                                                24-APR-2001;
30-APR-2001;
04-MAY-2001;
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08-DEC-2000;
24-JAN-2001;
16-MAR-2001;
          Sequence
                                                                                                                                                                                            The present invention relates to methods of detecting a prostate
                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                   Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
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                                ABG61800-ABG61944 represent prostate cancer-associated proteins
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                                                                                                                                                                                                                                                                                                                       Mack DH,
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2000US-0733742

2001US-26357P

2001US-276791P

2001US-281122P

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2001US-286589P
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Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS,
                                                     (SKEI/)
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Kalos MD; Carter D;

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Query Match
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
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14-JUL-1998;
23-SEP-1998;
15-JAN-1999;
                                                                  (RETT/)
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14-JAN-2000;
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DAY C H.
VEDVICK T S.
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KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                   HARLOCKER S L.
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HENDERSON R A.
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2000US-0431673

2000US-0558870

2000US-0558100

2000US-05597037

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100.0%; Pred. No. 1.3e-06;
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                                                                                                                                                                                                                                                                             03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                           Tang
Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatm of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
                                                             Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
                                                                                                             WPI; 2001-476283/51.
N-PSDB; AAK52962.
                                                                                                                                                                                                                                                                                                                                                                                                               05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; amunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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                             Claim 20; Page 350; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein SEQ ID NO 3475
                                                                                                                                                                                                                                                               30-NOV-2000;
                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
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                                                                                                                                                                           S.
                                                                                                                                                           , Liu C,
, Wang D,
Yang Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 879; 87pp; English.
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ilarity 100.0%;
Conservative (
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2000US-0560875
2000US-0598075
2000US-0620325
2000US-0620325
2000US-063561
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2000US-0693325
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Wang J, Zhang J, Ro
Wejhrman T, Goodrich
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                                                                                                                                                           , Asundi V, Zhou ;
Zhang J, Ren F, Ci
, Goodrich R;
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Pred. No.
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                                                                                                                                                                 u C,
Wang
                                                                               activities
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ng ZW;
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AAE02780
ID AAE02
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  PANCE TO THE PROPERTY OF THE P
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                               Domain
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encoded polypeptides (AAM/8233-AAM/80102) that exhibit activity elating to cycokine, cell proliferation or cell differentiation or which may induce production of other cycokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cycokine-like activities, epittem cell growth factor activity, hamanemodulatory activity and activity, insue growth factor activity, immunemodulatory activity and civity/inhibin activity and may be useful in the disgoses and/or restremen of cancer; leukaemia, nervous system disorders, arthritis and resultance.
                                                                                 Note: Records for SEO ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitred as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                    nflammation.
374 AA;
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1 WKMKPRRNLEEDDYL 15
                        Conservative
                                100.0%;
                        0
                              Score 86; DB 22;
Pred. No. 1.4e-06;
                        Mismatches
                                       Length 374;
                        Indels
                        0
                        Gaps
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Human six transmembrane epithelial antigen of prostate (STEAP)-1 protein.
                                                                                                    AAE02780 standard;
                                                                                                                                                                                           49 WKMKPRRNLEEDDYL
                                 (first entry)
                                                                                                    Protein;
                                                                                                                                                                                           63
                                                                                                    375
                                                                                                       ₽
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Human; cyrostatic; antiproliferative; vaccine; gene therapy six transmembrane epithelial antigen of the prostate-l; STEAP-l; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian; Homo sapiens. chromosome 7p22.3; pancreatic.

Misc-difference WO200140276-A2 262..270 Location/Qualifiers /label= Transmembrane\_domain #6 /label= HLA-A2\_binding\_peptide #3 158..166 /label= Immunogenic\_peptide #1 /label= label= Transmembrane\_domain #5 'label= HLA-A2\_binding\_peptide #: label= Tabe. label= Transmembrane\_domain #4 label= HLA-A2\_binding\_peptide #2 .340 . 241 184 310 l= Transmembrane\_domain #1 "Encoded by TTGTAGAAT" HLA-A2\_binding\_peptide Transmembrane\_domain #3 HLA-A2\_binding\_peptide #5 Transmembrane\_domain #2

The invention relates to polymucleotides (AAK51456-AAK53435) and the

(ESTs) for

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RESULT 13
ANY11840
ID ANY11840
XX
AC ANY11
XX
DY 18-JU
DY 18-JU
DX Human
XX
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                                                                                                                                                                                                                                                                                Human, secreted procein; EST, expressed sequence tog, diagnosis, foressis; gene therapy, chromosome mapping; signal psptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; upstream tation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemosatic; chemothetic, haematatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-367804/38.
N-PSDB; AAD07067.
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 5' EST secreted protein SEQ ID No: 440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY11840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY11840 standard; Protein; 95 AA.
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                           31-JUL-1998;
                                                                                      11-FEB-1999.
                                                                                                                                          WO9906550-A2
                                                                                                                                                                                                                                                        thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2000; 2000WO-US33040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                            anti-inflammatory; tumour inhibition.
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                               98WO-IB01232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimman secreted proteins expressed in prostate, and encode the proteins civen in ANXIIVAE to ANXIIVAE respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The unleic acid sequences can be used for producing secreted protein. The products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity. Cell transcription and differentiation activity, hashestation and differentiation activity, reproductive hormone cregulating activity, chemotactic/chemotactivity, anti-inflammatory cativity, tumour thibition activity, and activity, anti-inflammatory cativity, tumour thibition activity and activity. An products cativity in the products can be used in forensic, gene therapy and chromosome mapping promoter cative sequences. The nucleic acids encoding the signal peptides can be used for cativities of the products active the nucleic acids encoding the signal peptides can be used for cativity and activity activity and activity. The activity and activity and activity activities activity activity and activity and activity and activity activities activity. The activities activity activities activitie
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                           Cate RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-1999
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                                                                                                                                                                         23-MAY-1997;
                                                                                                                                                                                                                                                                                        26-NOV-1998.
                                                                                                                                                                                                                                                                                                                                               WO9853071-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kidney injury associated molecule HW018 protein
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                                                                                      (BIOJ ) BIOGEN INC.
                                                                                                                                          23-MAY-1997;
                                                                                                                                                                                                                                 22-MAY-1998;
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                           Hession CA,
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97US-0047490
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                               Sanicola-Nadel M,
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WPI; 1999-045312/04.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
                    Drmanac RT, Liu C,
                                                                                                                 31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                    WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #25508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABG25517 standard; Protein; 72 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 57-58; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                                                      11-OCT-2001.
                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 WKMKPKGNLEDDSY 27
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2000US-0649167.
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71.4%;
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cc polymeptide (II) sequences (II) is useful as hybridisation probes, cc polymerses chain reaction (PCD) primers, oligomers, and for chromosome can gene mapping, and in recombinant production of (II). The polymerses can be useful in deposition of (II). The complex complex can be useful in gene therapy techniques of ridentifying expressed genes. (II) is useful in gene therapy techniques (II) in the complex can be useful in gene therapy techniques (III) in the complex can be useful for generating antibodies against the detecting of comparities and the production of the services of the services are useful in medical can service as food supplement. (II) and its binding partners are useful in medical consisting of sites expressing (II). (II) and (III) are useful for treating disorders involving aberrant protein expression or biological activity of the polymeptide and polymulectide sequences have applications in consisting for the sequences, where mapping identification of materions are responsible for generic disorders or other traits to assess biodiversity assimply produce other types of data and reducted dependent on DNA and canino acid sequences of their thoughton. The suppose of the comparation of the printed specification, but was obtained in electronic format directly from NIPO
                       Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID No 55876; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-639362/73.
N-PSDB; AAS89704.
                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and
                                                                                                   72 AA;
                           52.3%;
; Score 45; DB;
; Pred. No. 3.1;
2; Mismatches
                                                   DB 22;
                                               Length 72
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Search completed: March 26, 2003, 16:48:00 Job time : 33.1279 secs

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39 WKLKPONNLPE 49 1 WKMKPRRNLEE 11 Similarity 7; Conserv

Matches

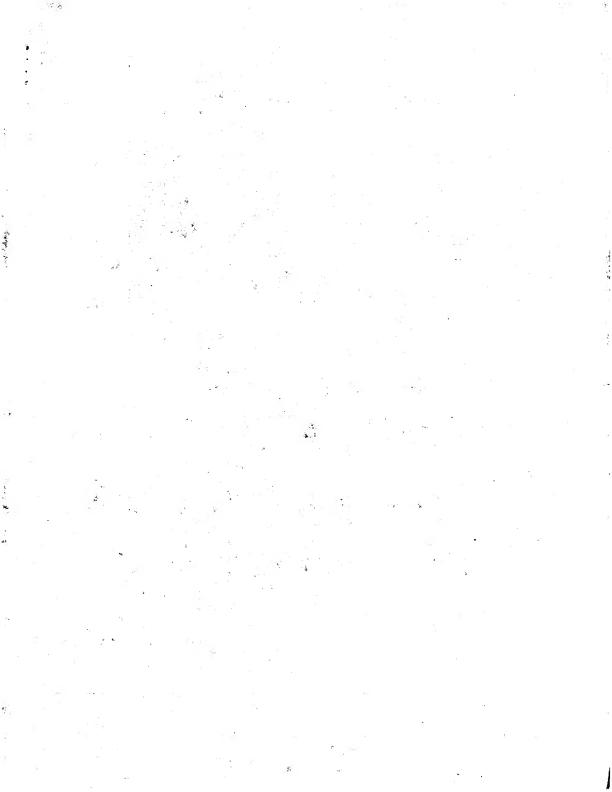
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Listing first 45 summaries
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Published Applications AA:*

1. /cgn2-6/ptcdata/1/pubpaa/USO8 NEW FUB.pep:*

2. /cgn2-6/ptcdata/1/pubpaa/USO8 NEW FUB.pep:*

3. /cgn2-6/ptcdata/1/pubpaa/USO8 NEW FUB.pep:*

4. /cgn2-6/ptcdata/1/pubpaa/USO8 NEW FUB.pep:*

5. /cgn2-6/ptcdata/1/pubpaa/USO9 NEW FUB.pep:*

6. /cgn2-6/ptcdata/1/pubpaa/USO9 NEW FUB.pep:*

7. /cgn2-6/ptcdata/1/pubpaa/USO9 PUBCOWB.pep:*

8. /cgn2-6/ptcdata/1/pubpaa/USO9 PUBCOWB.pep:*

9. /cgn2-6/ptcdata/1/pubpaa/USO9 NEW FUB.pep:*

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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	t Query Match Length	DB	ID .	Description
1	9.8	100.0	339	إ	US-10-012-896-879	Sequence 879, App
N	96	100.0	339	ø	US-09-802-520-11	Sequence 11, Appl
ω	86	100.0	339	ø	US-09-895-793-879	Sequence 879, App
4	86	100.0	339	ø	US-09-895-814-879	Sequence 879, App
ъ	98	100.0	339	ø	US-10-011-095-2	Sequence 2, Appli
6	86	100.0	339	ø	US-10-010-667A-2	Sequence 2, Appli
7	86	100.0	339	10	US-09-759-143-879	Sequence 879, App
8	86	100.0	339	10	US-09-780-669-879	Sequence 879, App
9	86	100.0	339	10	US-09-822-827-879	Sequence 879, App
10	42	48.8	1018	5	US-09-801-574-32	Sequence 32, Appl
11	42	48.8	1019	10	US-09-801-574-76	Sequence 76, Appl
12	39	45.3	262	ø	US-09-813-453A-45	Sequence 45, Appl
13	38	44.2	404	ø	US-09-486-734A-12	Sequence 12, Appl
14	38	44.2	539	10	US-09-815-242-10497	Sequence 10497, A
15	38	44.2	968	10	US-09-753-008-7	Sequence 7, Appli
16	37.5	43.6	405	ø	US-10-102-806-675	Sequence 675, App
17	37.5	43.6	803	ø	US-09-968-436B-2	Sequence 2, Appli
18	37.5	43.6	803	10	US-09-759-010-7	Sequence 7, Appli
19	37	43.0	46	10	US-09-864-761-34052	Sequence 34052, A

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37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
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US-10-101-464A-932	US-09-860-298-2	US-10-141-755-160	US-10-121-050-160	US-10-142-423-160	US-10-123-262-160	US-10-142-419-160	US-10-140-002-160	US-10-143-114-160	US-10-142-431-160	US-10-140-474-160	US-10-137-865-160	US-10-176-921-160	US-10-176-918-160	US-10-175-746-160	US-09-832-129-37	US-10-140-470-160	US-10-123-904-160	US-10-121-049-160	US-10-028-072-160	US-09-893-519A-61	US-09-817-764-3	US-09-746-783-66	US-10-078-650-14	US-09-925-302-448	US-10-078-650-18
Seguence 932, App	Sequence 2, Appli	Sequence 160, App	Seguence 160, App	Sequence 37, Appl	Sequence 160, App	Sequence 160, App	Sequence 160, App	Sequence 160, App	Sequence 61, Appl	Sequence 3, Appli	Sequence 66, Appl	Sequence 14, Appl	Sequence 448, App	Sequence 18, Appl											

### ALIGNMENTS

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							-10	CURRENT APPLICATION NUMBER: US/10/012,896		0	COMPOSITIONS AND METHODS	Madeleine Joy	iro				۲			P	•	•				•						5	ŗ				-	Sequence 879, Application US/10012896	
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Matches Query Match Best Local :

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Conservative

Mismatches

Indels

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Gaps

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9.5e-07; DB 9; Length 339; 0

Local Similarity

100.0%; Score 86; o,

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FEATURE:
; NAME/KRY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
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SEQ ID NO 11
LENGTH: 339
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FILE REFERENCE: PC-037 US
CURRENT APPLICATION NUMBER: US/09/802,520
CURRENT FILING DATE: 201-03-09
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lal, Preeti
APPLICANT: Faris, Mary
APPLICANT: Chen, Huei-Mei
APPLICANT: Ison, Crain
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
                              APPLICANT: FOY, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: ONEOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/895,793
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ORGANISM: Homo sapiens
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Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Kalos, Michael D.
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Hepler, William T.
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Carter, Darrick
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ilarity 100.0%; Pred. No.
Conservative 0; Mismatch
                                                                                                                                                                                                                                                        , Samuel X.
                                                                                                                                                                                                                                    Aijun
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9.5e-07;
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                                                                                                                         US-09-895-814-879
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                                                                                                                                                                                 APPLICANT: FRAIGE, GATY R.

TITLE OF INVENTION: CHOPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER.

FILE REFERENCE: 21012, 447C26
CURRENT PAPPLICATION NUMBER: US/99/895, 814
CURRENT PAPPLICATION NUMBER: US/99/895, 814
CURRENT PAIRO DATE: 2001-06-29
SUPTHARE: PROTESSO TO WINDOWS Version 3.0
SEQ TD NO 879
SOFTHARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 982
SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 879
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                                                              Matches
                                                                          Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TYPE: PRT
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                                                                                                                                                                      LENGTH: 339
  14 WKMKPRRNLEEDDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 WKMKPRRNLEEDDYL 28
                       1 WKMKPRRNLEEDDYL 15
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                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Day, ... Thom... Vedvick, Thom... Carter, Darrick Li, Samuel X. Aijun
                                                                                                                                                                                                                                                                                                                                       McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Kalos, Michael D.
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Hepler, William T.
Henderson, Robert A.
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                                                              Conservative
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                                                                          100.0%;
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28
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                                                                          Score 86; DB 9;
Pred. No. 9.5e-07;
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Pred. No. 9.5e-07;
                                                                Mismatches
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                                                                                            Length 339;
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                                                           Gaps
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US-10-011-095-2
, Sequence 2, Application US/10011095
, Publication No. US20030045682A1
, GENERAL INFORMATION:

APPLICANT: Afar, Daniel

RESULT 5

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APPLICANT: BENLY NAME: APPLICANT: RAILEND, Arthur B.
APPLICANT: Saffran, Douglas C.
APPLICANT: Saffran, Douglas C.
APPLICANT: Matchell, Steve Chappell
TITLE OF INVENTION: NOVEL SEREENTHE THANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREO
FILE REFERENCE: 511582001601
GURRENT APPLICATION NUMBER: US/10/010,667A
GURRENT APPLICATION NUMBER: 09/323,873
PRIOR FILLING DATE: 199-06-01
PRIOR PRICHION DATE: 199-06-01
PRIOR PRICHION NUMBER: 60/097,520
PRIOR PRICHION NUMBER: 60/097,520
PRIOR PRICHION NUMBER: 60/097,520
PRIOR PRICHION DATE: 199-06-01
PRIOR PRICHION DATE: 199-06-01
PRIOR PRICHION DATE: 199-06-01
PRIOR PRICHION DATE: 199-06-01
PRIOR PRICHION NUMBER: 60/091,183
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US-10-011-095-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
SEQ ID NO 2
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Best Local :
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APPLICANT: Mitchell, Steve Chappell
TITLE OF INVESTIGN. STEVE CHAPPLICANT: MITCHELL, Steve Chappell
TITLE OF INVESTIGN: ANTIBOLIES INVINOSPECIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 511582001610
CURRENT APPLICATION NUMBER: 09/10/011,095
CURRENT PILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR PILING DATE: 1999-06-10/087,520
PRIOR APPLICATION NUMBER: 06/087,520
PRIOR APPLICATION NUMBER: 06/081,183
PRIOR PILING DATE: 1999-06-10/081,183
PRIOR PILING DATE: 1999-06-10/081,183
PRIOR PILING DATE: 1999-06-10/081,183
PRIOR PILING DATE: 1999-06-10/081,183
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APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                          LENGTH: 339
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                                                                                                                          Local Similarity
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                               1 WKMKPRRNLEEDDYL 15
WKMKPRRNLEEDDYL 28
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Leong, Kahan
                                                                                                     Conservative
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                                                                                                                          100.0%; Score 86; DB 9;
100.0%; Pred. No. 9.5e-07;
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APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21012.1.427C33
CUMRENT APPLICATION UNDERS: US/09/759,143
CUMRENT APPLICATION UNDERS: US/09/759,143
CUMRENT OF SEQ ID NOS: 934
MUMBER OF SEQ ID NOS: 934
MUMBER OF SEQ ID NOS: 934
SOFTMARE: PRESEEQ FOR WINDOWS Version 3.0
SEQ ID NO 879
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. US20020051977A1
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APPLICANT:
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                        APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
HITE REFERENCE. 2012/14/2004
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CURRENT APPLICATION NUMBER: US/09/780,669
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o. US20020022248A1
                                                                                                                                                                                                       Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
                                                                                                                                                                                      Day, Craig H.
Vedvick, Thomas
Carter, Darrick
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Vedvick, Thomas
Carter, Darrick
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Retter, Marc W.
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ick, Thomas S.
                 210121.427C24
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                                                                                                                                                                                                                                                                                                                  Robert A.
                                                                                                                                                                                                                                                                                                                                               Susan L.
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; LENGTH: 1018
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-801-574-32
                                                                                                                                                                                                                                                 APPLICANT: Wang Pediing Jeremy
APPLICANT: Page David C.
TITLE OF INVENTION: Reproduction-Specific Genea
FILE REFERENCE: 0399:2007-002
CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT PILING DATE: 2001-03-07
PRIOR APPLICATION WIMBER: 60/187,518
PRIOR APPLICATION WIMBER: 60/261,557
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2001-01-12
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US-09-780-669-879
                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 86; Best Local Similarity 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 879, Application US/09822827
Patent No. US20020081680A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 879
                            Matches
                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 32, Application US/09801574
Patent No. US20020081592A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: XU, JIANGCHUN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION UNMER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2001-02-09
                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 339
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 WKMKPRRNLEEDDYL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 WKMKPRRNLEEDDYL 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                         Conservative
                                              48.8%;
53.8%;
                         Score 42; DB
Pred. No. 73;
2; Mismatches
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                                                                  DB 10; Length 1018;
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                         4
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                            Indels
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; LENGTH: 1019
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-574-76
RESULT 13
US-09-486-734A-12
; Sequence 12, Application US/09486734A
                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang Pediing Jeremy
APPLICANT: Page David C.
TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002 /05/801,574
CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2001-01-12
NUMBER OF DEED ID NOS: 90
SOFTMARE: PastSEO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45
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                                                                                                                                                                                                                                                                                                                                                                                                 MEDILICANT: YOCUM, R. ROGETS
APPLICANT: YOCUM, R. ROGETS
APPLICANT, PRITETERS, THOMAS A.
TITLE OF INVENTION: MICHOORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
TITLE OF INVENTION: MATHEMOTICS
FILE REFERENCE: OG2-O10
CURRENT APPLICATION NUMBER: US/09/813,453A
CURRENT APPLICATION NUMBER: US/09/813,453A
CURRENT PILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: US/67/27,860
PRIOR APPLICATION NUMBER: US/67/569
PRIOR APPLICATION NUMBER: US/687,569
PRIOR APPLICATION NUMBER: US/687,569
PRIOR APPLICATION NUMBER: 09/687,569
PRIOR APPLICATION NUMBER: US/687,569
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Best Local
                                                                                                                                                                                                                                                                                               LENGTH: 262
TYPB: PRT
ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         645 WKLVEKSNLEESD 657
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                                                                                                             26
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nes 7; Conserv
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                                                                                                                                                     1 WKMKPRRNLEEDDY 14
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                                                                                                             WRMETDRHKTEDEY 39
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                                                                                                                                                                                              Conservative
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Pred. No. 74;
2; Mismatches
                                                                                                                                                                                                                  Score 39;
Pred. No.
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                         9
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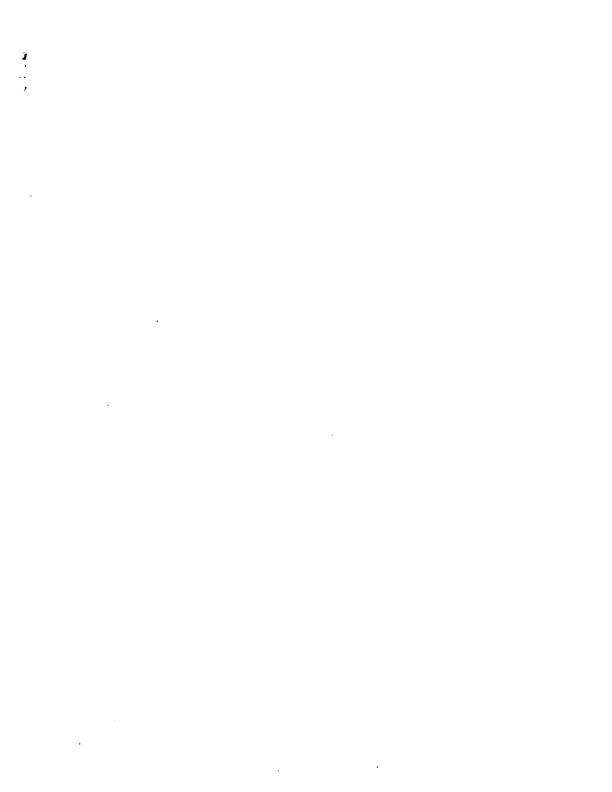
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; ORGANISM: Enterococcus faecalis US-09-815-242-10497
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US-09-815-242-10497
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LENGTH: 404
TYPE: PRT
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                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10497
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Best Local Similarity 42.9%;
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CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCTP898/01873
PRIOR FILING DATE: 1996-09-01
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEG ID NGS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITEA, 011A
CURBENT APPLICATION UNBER: US/09/815,242
CURENT FILING DATE: 2001-03-21
PRIOR APPLICATION UNBER: 60/91,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Erlich, S. Dusko
APPLICANT: Gattier, Michel
APPLICANT: Schouler, Catherier
APPLICANT: Schouler, Catherier
APPLICANT: Schouler, Catherier
APPLICANT: Institut Mational de la Recherche Agronomique
APPLICANT: Institut Mational de la Recherche Agronomique
TITLE OF INVENTION: Bacceriophages of Lactic Acid Bacceria
FILE REFERENCE: 33339/19648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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APPLICANT: Clier, Florence
                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Lactococcus lactis
                                                                    LENGTH: 539
                                                                                                                                                      OR APPLICATION NUMBER: 60/242,578
OR FILLING DATE: 2000-10-23
OR APPLICATION NUMBER: 60/253,625
OR FILLING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILLING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/269,308
OR FILLING DATE: 2001-02-16
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FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert T.
Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind, Judith W. Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 1.2e+0;
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DESCRIPTION: peptide
HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-753-008-7
밁
                                                   Query Match
Best Local Similarity
Watches 6; Conserve
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US-09-753-008-7
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Best Local
                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 697-5995
TELEPAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-591-4766
INFORMATION FOR SEQ ID NO. 7
SEQUENCE CHARACTERISTICS:
293 WKMQPSNQTEADN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

PROGRAPHICATION NUMBER: 09/385,752
APPLICATION NUMBER: 09/385,752
PILING DATE: 1999-08-30
APPLICATION NUMBER: 09/651,999
PILING DATE: MAY 22, 1996
APPOREEY/AGENT INFORMATION:
REGISTRATION NUMBER: 39,911
REGISTRATION NUMBER: 39,911
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                                 1 WKMKPRRNLEEDD 13
                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 I
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APPLICATION NUMBER: US/09/753,008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICAMT: Stefan Somlo and Toshio Mochizuki
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE PKD2 GENE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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7; Conserv
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SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: AMSTER, ROT
STREET: 90 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 96700/395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: NEW YORK
                                                                                                                                                                                                                                                                                             ENGTH: 968 amino acids
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                                                                        Conservative
                                                                     44.2%; Score 38; DB 10; Length 968;
46.2%; Pred. No. 3.2e+02;
ative 2; Mismatches 5; Indels
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DISKETTE
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Pred. No. 1.7e+02;
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Search completed: March 26, 2003, 17:04:14 Job time : 11.1163 secs



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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: sp_archea:*
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Gapop 10.0 , Gapext 0.5
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86
1 WKMKPRRNLEEDDYL 15
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                                                                                                       sp_organelle:*
sp_phage:*
sp_plant:*
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sp_unclassified:*
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sp_archeap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	<b>œ</b>	7	ō	<sub>5</sub>	4	ω	2	٦	Result
42	43	43	43	44	44	44	44	45	45	45.5	63	63	63	67.5	78	Score
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1 WKMKPRRNLEEDDYL 15

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## ALIGNMENTS

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O Q9Y6U5 PRELIMINARY; PRT; 264 AA.	
1999 (TrEMBLrel.	
(TrEMBLrel. 12,	
, Last	
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Chordata;	
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
SEQUENCE FROM N.A.	
K MEDLINE=99063792; PubMed=9847074;	
Sulston J.E., Waterston R.;	
r "Toward a complete human genome sequence.";	
Genome Res. 8:1097-1108(1998).	
N [2]	
SEQUENCE FROM N.A.	
Strong C., Layman D., Graves T., Strowmatt C.;	
"The sequence of Homo sapiens BAC clone CTB-87E15.";	
יייי משחוררבת (סטא-1930) רס רווב פאופא/ שפוומווא/ שטפט תמרמאמפבפי	
SEQUENCE FROM N.A.	
R.,	
L Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.	
R EMBL; AC005061; AAD43182.1;	
r NON_TER 1 1	
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JENCE 264 AA;	
90.7%; Score 78;	
cal Similarity 86.7%; Pred. No. 1.7e-05;	
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps	

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RA Arzawa K., Izawa M., Kiyoswa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
RA Aslico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Relafenhann W., Gasterland T., Gissi C., King B., Kochwa H.,
RA Fleischmann W., Gasterland T., Gissi C., King B., Kochwa H.,
RA Fleischmann W., Gasterland T., Wilde G., Okackenhush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Garinci P., de Bonaldo M.F.,
RA Schriml L.M., Staubli C., Fletcher C., Fujita M., Garinci P.,
RA Brownstein M.J., Sult C., Fletcher C., Fujita M., Godone C.,
RA Brownstein M.J., Sult C., Fletcher C., Fujita M., Godone C.,
RA Gustinctio S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Mordone P., Ring B., Kingwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch X.-F.,
RA Mordone P., Ring B., Kingwald K.H., Weitz C., Whittaker C., Wilding L.,
RA Myrahaw-Borla A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Matches 13
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09CMR7, 01-JUN-2001 (TERNBLEG). 17, C

01-JUN-2001 (TERNBLEG). 17, L

01-JUN-2001 (TERNBLEG). 19, L

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STEAP OR 241007B19RIX.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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Ol-MAR-2001 (TEMBLIEL 16, Last annotation update)
Six transmembrane endothelial antigen of PAEC.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUB=EMBRYONIC STEM CELLS;
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                                   "Functional annotation of a Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
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Rodentia;
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                                                              full-length mouse cDNA collection.";
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                                                                                                                                                                                                                       MEDILINE-21371909; PubMed=11479226;
Yang D. Holl G.B., Velders M.P., Kwon E.D., Kast W.M.;
Yaurine six-transmembrane epithelial antigon of the prostate, prostate
stem cell antigon, and prostate-specific membrane antigon; prostate-
specific cell-surface antigons highly expressed in prostate cancer of
                                                                                                                                                                 transgenic adenocarcinoma mouse prostate mice."; Cancer Res. 61:5857-5860(2001).
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                                   SEQUENCE
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                                                                                                       MGD; MGI:1917608; Steap.
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Matches 10
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01-DEC-2001
01-DEC-2001
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SEQUENCE 339 AA; 39264 MW;
                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                         of human STEAP.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL, AV029584; AAK50537.1;
MGD; MGI:1915678; 1010001D01Rik.
                                                                                                         01-DGC-2001 (TEXMBLRE1. 19, Created)
01-DGC-2001 (TEXMBLRE1. 19, Last sequence update)
01-UNN-2002 (TEXMBLRE1. 21, Last annotation update)
Six-transmembrane epithelial antigen of the prostate.
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Mammalia; Eutheria;
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STRAIN=C57BL/6;
           SEQUENCE FROM N.A.
                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Prostate and non-prostate expression of dudulin, the mouse ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Serru V., Manivet P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                   Score 63;
Pred. No.
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Pred. No.
                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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0.009;
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                                                     Muridae; Murinae; Mus
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Best Local Similarity
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Best Local
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Barrell B.G., Rajandream M.A., McDougall R.C., McLean J., Herris D.;
Bubmitted (NOY-1999) to the EMBL/GenBank/DDBJ databases.

MMBL; ML131225; CAB61781.1;
Interpro, ITMO0327; DUF207:

Hypothatical protein.

Hypothatical protein.

SEQUENCE 237 AA; 26997 MM; 29A6CF0D0C720997 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8XDR7;
01-MAR-2002
01-MAR-2002
                                                                                                                         STRAIN-0157H7 / EDL933 / ATCC 700927;

MEDLINE-21074955 PubMed-11205551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck B.J., Davis M.W., Lim A., Dimalanta B.T., Potemousis K.,

Apodaca J., Anatharanan T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.,

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-MAR-2002 (TEEMBLrel. 20, Created)
Ol-MAR-2002 (TEEMBLrel. 20, Last sequence update)
Ol-UN-2002 (TEEMBLrel. 21, Last annotation update)
RNBase D, processes tRNA precursor.
RND 08 Z2847 07 RECS2513.
Escherichia coli 0157.H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conserved hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9UTA5;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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                         STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBI_TaxID=83334;
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   T., Makino
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71.4%;
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   Ohnishi M.,
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Pred. No.
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Kurokawa K.,
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   Ishii K.,
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   Yokoyama K.,
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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                                                                    01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2002 (TrEMBLrel. 20,
Activated protein kinase C:
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EMBL; AP002558; BAB35936.1;
InterPro; IPR002562; 3_5_exc
                              Trypanosoma vivex.
Bukaryotea Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5899;
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EMBL, AP00254; BAB07964.1; -
SEQUENCE 2058 AA; 226376 MW; BA06B6562B8BBD69 CRC64;
                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                      Enkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
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P0406H10.14.
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SMART; SM00341; HRDC; 1.
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SEQUENCE FROM N.A.
STRAIN=ILDAT1.2;
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STRAIN=CV. NIPPONBARE;
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InterPro; IPR002121; HRDC
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Pred. No.
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Pred. No.
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Best Local S
Matches 10
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Best Local S
Matches 7
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080941; ORD (TEMBLE) 08, C.
01-NOV-1998 (TEMBLE) 08, L.
01-NOV-1998 (TEMBLE) 18, L.
01-DEC-2001 (TEMBLE) 19, L.
AL2937730 protein.
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PRODEM; PR0001019; MD40; 4.

SMART; SM00120; MD40; 7,

PROSITE; PS00679; MD REPEATS 1; UNKNOWN 3.

PROSITE; PS00679; MD REPEATS 2; 5.

PROSITE; PS00294; MD REPEATS REGION; 1.

Kiname; Receptor; Repeat; MD repeat.

SEQUENCE 3: 7 AA; 34895 MM; B3CFB35D520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-20083487, PubMeda-1067197,
Lin X., Kaul B., Rounardy S.D., Shea T.P., Benito M.-I., Town C.D.,
Pdyli C.Y., Wason T.M., Bowman C.L., Barneteed M. E., Peldylym T.V.,
Buell C.R., Ketchum K., Lee J.J., Ronning C.M., Koo H., Moffet K.S.,
Cronin L.A., Shan M. Vunken S.E., Umayam L. Tallon L.J., Gill J.E.,
Adama M.D., Carrers A.J., Creast T.H., Goodman H.M., Sometrille C.R.,
Copenhaver C.P., Preuss M., Vencer J.C., White O., Eisen J.A.,
Salaberg S.L., Fraser C.M., Vencer J.C., White O., Eisen J.A.,
Salaberg and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- SIMILARITY: CONTAINS 7 MD:
EMBL; AF100287; AAC72850.1; --
InterPro; IPR001680; MD40.
Pfam; PF00400; WD40; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Bukaryota (Viridiplantae) Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledoms; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL, ACC04684, AAC23643 1; 157066866846B4ES CRC64; SEQUENCE 332 AA; 60372 MW; 157066866846B4ES CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 402:761-768(1999).
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                                                                                                                            476 WKMAPRRQCCEIVNSEED 493
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                                                                                                                                                                                               WKMKPRR----NLEED 12
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                                                                                                                                                                                                                                                                                         Score 44;
Pred. No.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                        Length 532;
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RESULT
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Best Local
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076517;
01-NOV-1998
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01-DEC-2001
01-DEC-2001
01-JUN-2002
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Kelley R.J., Alexander D.L., Cowan C.,
"Molecular cloning of p67, a lysosomal
Trypanosoma brucel";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002936; DNAprim_toprim.
InterPro; IPR002380; Prok_tpisomrase.
Pfam; PP01131; Toprim; I
Pfam; PF01751; Toprim; I
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Selbitschka W.,
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Bacteria; Proteobacteria; alpha
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGRFAM8;
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                                                                                                                                                                                                                                                              Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                           773 AA;
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(TrEMBLrel.
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Pred. No. 37;
2; Mismatches
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                                                                                                                                                                                                                                                                                         Score 44; DB
Pred. No. 44;
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MAÎ. BJOChem. Parasicol. 98:17-28(1999).

EMBI, ARO74657, AAC2845611 - .
InterPro; IRRO01064; Crystallin.

PROSITE; PRO0225; CRYSTALLIN BETAGAMMA, UNKNOMN 1.

SEQUENCE 659 AA; 72704 MW; 4E96EE5C81C06993 CRC64;
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01-NOV-1998 (TEMBLIRE). 08, Last sequence update)
01-DEC-2001 (TEMBLIRE). 19, Last amnotation update)
Lyacsomal/endosomal membrane protein p67.
Trypanosoma brucei rhodesiense.
                                                                                                                                                                                                                                                                                  "The genetic organization and evolution of the broad-host range marcury resistance plasmid pSBUO isolated from a microbial population residing in the chicosphace of alfalia.", Submitted in the chicosphace of alfalia.", Submitted (DEC-2000) to the BMBL/GenBank/DDBJ databases.

BMBL/AJ0433; CAC79183.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schneiker S., Keller M., Droege M., Lanka E., Pu
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NCI_TaxID=31286;
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Last annotation update)
                                                                                                       DBE36F5AC6F20E68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subdivision; Rhizobiaceae group;
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5
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RESULT 14
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Q94HS8;
01-DEC-2001 (TremBLrel. 1
01-DEC-2001 (TremBLrel. 1
01-JUN-2002 (TremBLrel. 2
                                      Hypothetical protein.
Oryza sativa (Rice).
Oryza sativa (Rice).
Sukaryora; Viridiplantas; Streptophyra; En
Spermatophyra, Magnollophyra; Lillopeida;
Ehthartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R. Ainscough R. Anderson K., Baynes C., Berks M., Bonfield J., Button J., Connell M., Copesy T., Cooper J., Coulson A Bonfield J., Button J., Connell M., Copesy T., Cooper J., Coulson A Craxton M., Dear S., Du Z., Durbin R., Favello A., Falton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Karsten J., Latster N., Lattrellle P., Lightning J., Lloyd C., McMurray A., Mortinore B., O'Callaghan M., Lightning J., Lloyd C., McMurray A., Mortinore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I Smaldon M., Smith A., Sonnhammer B., Staden R., Sulston J., Thonas K., Vaudin M., Vaughan K., Materston R., Watson A., Weinstock L., Wilkinson-Sproat J., Mohidman P., Materston R., Watson A., Weinstock L., Wilkinson-Sproat J., Mohidman P.,
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Q17557;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
SEQUENCE FROM N.A. Wing R.A., Frisch
                                                                                                                                                                                                                                                                                                 InterPro; IPR000340; DS phosphatase.
InterPro; IPR000366; Lipoclin_CytPABP.
InterPro; IPR003782; SCO1_SenC.
Pf4m; PF02630; SCO1_SenC; 1.
SMART; SM0012; PTPC_DSTG; 1.
PROSITE; PS010213; LIFOCALIN; UNKNOWN.
                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U58761; AAB00716.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                   "The sequence of C. elegans cosmid COIF1.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnson D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                              NCBI_TaxID=4530;
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7; Conserv
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Presting G.,
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Pred. No.
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                                                                                                                                          PRT;
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a; Poales; Poaceae;
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 Soderlund
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Pfam; PF00646; F-box; 1.
PROSITE; PS50181; FBOX; 1.
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HSSP; P02751; 2FN
MEROPS; M10.004;
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MAYAZAK K., UCHİYAMA K., IRONAWA Y., YOSHİZALO K.;
"Cloning and characterization of CODNAs for matrix metalloproteinases
of regenerating newt limbs.",
Proc. NALL. Acad. Sci. U.S.A., 93:6819-6824 (1996).
1- FUNCTION: COULD PLAY A ROLE IN BONE OSTECCLASTIC RESORPTION. MAY
BE INVOLVED IN TISSUE REMODELLING OF THE REGENEATING LING LANG.
1- CATALYTIC ACTIVITY: CLEAPAGES OF GELATIN TYPES I AND V AND COLLAGE
1- CATALYTIC ACTIVITY: CLEAPAGES OF GELATIN TYPES I AND V AND COLLAGE
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01-FEB-1997 (TERMILTEL 02, Created)
01-FEB-1997 (TERMILTEL 02, Last sequence update)
01-EEC-2001 (TERMILTEL 15, Last amovastion update)
92 kba type IV collagenase precursor [EC 3.4.24.35) (92 kba
gelattinase) (Matrix metalloproteinase 9) (MWP-9) (Gelatinase B).
Cynops pyrrhogaster (Japanese common newt)
Suharyota; Metacos, Choddata; Stamandroides; Salamandridae; Cynops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=REGENERATING LIMB BLASTEMA; MEDLINE=96270627; Pubmed=8692902;
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InterPro; IPR000585; Hemopexin.
InterPro; IPR001818; Matrixin.
InterPro; IPR000130; Zn_MTpeptds
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SIMILARITY: THE CENTRAL DOWALN SHOWS SIMILARITY TO THE TYPE-II
MOTIF OF COLLAGEN-BINDING DOMAIN OF FIERONECTIN. THIS DOMAIN B
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SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE II-LIKE DO
SIMILARITY: BELONGS TO EEPTIDASE FAMILY MIOA (ZINC
METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
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Search completed: March 26, 2003, 16:49:42 Job time: 20.6977 secs

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HOL. Gen. CLEAVES MULTIMERIC TRUM PR
- I - FUNCTION: CLEAVES MULTIMERIC TRUM PR
- I - CATALYTIC ACTIVITY: Endonucleolytic
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39.6 min of the chromosomal map and is a new member of the
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J. Bacteriol. 179:3004-3012(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE AUTOINDUCER SYNTHETASE FAMILY.
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                                                       sensing; Autoinducer synthesi
SE 193 AA; 22127 MW; 238E7
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7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Serotype Ol;
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(Rel. 40, Last sec
(Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthesis
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Last annotation update)
       51.2%; Score 44;
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Pred. No.
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                                                              238E760CD8701188 CRC64;
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       DB 1;
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SCHPO
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01428; 09UTX5;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 41, Last sequence update)
15-UN-2002 (Rel. 41, Last amoration update)
"Marge-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).

1- FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT ACTS UPON TRR1 AND CTY1.

1- SUBSCLULTAR LOCATION: Nuclear (Potential) BLONGS TO THE HSP FAMILY.

1- SIMILARITY: IN THE N-TERMINUL SECTION; BLONGS TO THE HSP FAMILY.

1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
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MEDLINE=9279565; PubMed=10348908;
Ohmiya R., Kato C., Yamada H., Alba H., Mizuno T.;
"A fisation yeast gene (prr1(+)) that encodes a response regulator implicated in oxidative stress response.";
J. Biochem. 125:1061-1066(1999).
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                                                                                                                                                                                                                      MEDLINE=20223868; PubMed=10759889; Ding D.Q., Tomita Y., Yamamoto A.,
                                                                                                                                                                                                                                                                                                 SEQUENCE OF 224-413
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                                                                                                                                                                                                                                                                                                 FROM N.A.
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4; Mismatches
                                                                                                                                                                                                                          Chikashige Y., Haraguchi T.,
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01-MAY-1991
01-MAY-1991
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Ol-MAY-1991 (Rel. 18, Last sequence update)
Ol-MAY-1991 (Rel. 18, Last sentence update)
Ol-MAY-1991 (Rel. 14, Last sentence component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2) (S complex, 48 KDa subunit).
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SEQUENCE
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PYODOM; PD000039; Response reg;
PYODOM; PD0001788; HSF DNA bind;
SMART; SM00415; HSF; 1.
SMART; SM00448; REC; 1.
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INGERPO, IPRO00232; HSP_DNA_bind.
INTERPO; IPRO02341; HSP_ETS.
INTERPO; IPRO01789; Response reg.
INTERPO; PFR00172 response reg.
Ffam; PF00047; HSP_DNA-DING; I
Pfam; PF00047; HSP_DNA-DING; I
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PROSITE, PS0110; RESPONSE REGULATORY; 1.
Transcription regulation; Sensory transduction; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB041768; BAB16722.1; -.
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SEQUENCE FROM N.A.
                                                               Microbiology 142:3033-3037(1996)
                                                                                                    winters P., Caldwell R., Entiald L., Perrari E.;
"The ampS-mprE (124 degrees-127 degrees) region of the
subrills 168 thromosome: sequencing of a 27 kb segment
identification of several genes in the area.";
                                                                                                                                                                                                                                                                                                                                                                                                                Hemila H., Palva A., Paulin L., Arvideon S., Palva I.; "Secretory S complax of Bacilius subtilis: sequence analysis and identity to pyruvate dehydrogenase."

J. Bacteriol. 172:5052-5053(1990)."
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NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                       MEDLINE=97124187; PubMed=8969500;
                                                                                                                                                                                                                                                                                                 STRAIN-168
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168
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9; Conserv
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539 AA;
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PHOSPHORYLATION (BY SIMILARITY)
F3B4945C595B2871 CRC64;
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STRAIN=168; Caldwell R.M.,

analysis of

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**Bubtilia** 

Ferrari

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Matches 7
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Q99024;
15-DEC-1998
15-DEC-1998
15-DEC-1998
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                                                                                                                                   TRIRE
                                                                                                                                                                                                                                                                                         DOMAIN
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBH outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is no removed. Usage by and for commercial entities requires a license spreament (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M57435; AAA62683.1; -. EMBL; AF012285; AAC24934.1; -. EMBL; Z99111; CAB13333.1; -. PIR; D36718; D36718.
                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                        Glycolysis; Transferase; Acyltransferase; Lipoyl; Complete proteome INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through
   Hypocreales;
                Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                           Trichoderma reesei (Hypocrea jecorina)
                                                    Alpha-glucuronidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subtilist; BG10209; pdhC.
                                                                                                                                                                                    21
                                                                                                                                                                                                                                      Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COFACTOR.
- SUBUNIT: E
SYMMETRY.
                                                                                                                                                                                                           1 WKMKPRRNLEEDDYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THE B.SUBTILIS PDH COMPLEX POSSESSES ALSO BRANCHED-CHAIN 2-OXOACID DEHYDROGENASE (BCDH) ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: The pyruvate dehydrogenase complex catalyzes the over-
conversion of pyruvate to acetyl-CoA and CO(2). It contains
multiple copies of three enzymatic components; pyruvate
dehydrogenase E1), dihydrolipamide acetylrransferase (E2) and
lipamide dehydrogenase [83).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE 2-OXOACID SIMILARITY: CONTAINS 1 LIPOYL-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetyldihydrolipoamide.
                                                                                                                                                                                    WFVKPNDEVDEDDVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                          441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORMS A 24-POLYPEPTIDE
                                                                                                                                                                                                                                      Conservative
   Hypocreaceae; Hypocrea.
                                                                                                                     STANDARD;
                                                    37, Created)
37, Last sequence update)
37, Last annotation update)
se precursor (EC 3.2.1.139)
                                                                                                                                                                                                                                                                                         47407 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIPOYL-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                LIPOYL BINDING.
E1/E3 BINDING.
LIPOYL.
                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                               Score 42;
                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                         6B44D47879D134DF CRC64;
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                                                      (Alpha-glucosiduronase)
                Sordariomycetes;
                                                                                                                                                                                                                                      5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ex catalyzes the overall
                                                                                                                                                                                                                                                               Length 441;
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Best Local
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15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The alpha-glucuronidase encoding gene of Trichoderma reessi.", Gene 172:171-172(1996).
                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SMISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the Enropean Bioinformatics Institute. There are no restr
                                               WEDLINE-21175/48; PubMed-11279525;
Wang P.J., McCarrey J.R., Yang F., Page D.C.;
"An abundance of X-linked gense expressed in spermatogonia.";
"An abundance of X-111Ked gense expressed in spermatogonia.";
Nat. Genet. 27:422-426(2001).
1- CRYALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
1- TISSUE SPECIFICITY: Testis-specific. Expressed only in male germ
                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96257277; PubMed=8654984;
Margolles-Clark E., Saloheimo M.,
                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                  Serine/threonine protein kinase 31 (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                             108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE STRAIN=QM9414 / Rut C-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=51453;
                                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interPro;
                                                                                                                                                                                                                                                                                                                                                                    2 KMKPRRNLEEDDY
           SIMILARITY: BELONGS TO THE SER/THR E SIMILARITY: CONTAINS 1 TUDOR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    + D-glucuronate,
SUBGELIULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: RELEASES 4-O-METHYLGLUCURONIC ACID CATALYTIC ACTIVITY: An alpha-D-glucuronoside
                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                           KLSPKLNLKEDGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            degradation;
                                                                                                                                                                                                                                                                                                                                                                                          7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR005154; Glyco_hydro_67.
03648; Glyco_hydro_67; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           847
                                                                                                                                                                                                                               (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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52
238
321
353
586
692
740
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                  STANDARD;
                         BELONGS TO THE SER/THR FAMILY OF
                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      48.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
Pred. No.
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N-LINKED
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(GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 847
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                          PROTEIN KINASES
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(POTENTIAL)
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                                                                                                                                                                        Murinae; Mus.
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Query Match
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(9EXUII, 09EXHH;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Seting/Parco (Rel. 41, Last sanotation update)
Seting/Parco (Rel. 41, Last sanotation update)
protein kinase NYD-SPK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the EMBL posterior on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Unage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenses/sb-sib.ch).
"Cloning of a new protein kinase gene related development."
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ |- OATRANTIC ACTIVITY: ATP + a protein = ADP |- TISSUB SPECIFICITY: Testis specific. |- SIMILARITY: BELONGS TO THE SER/TER FAMILY |- SIMILARITY: CONTAINS 1 TUDOS COMAIN.
                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50011; PROTEIN KINASE_DOM; 1. PROSITE; PS50304; TUDOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Euk pkinase; SMART; SM00220; S TKC; 1.
SMART; SM00333; TUDOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.
Pfam; PF00567; TUDOR; 1.
                                                                                                              Zhou
                                                                                                                                                                                                        Wang
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InterPro; IPR001097; Maternal_tudor.
InterPro; IPR000080; SNase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF285580; AAK31959.1; -.
                                                                                                                             TISSUE=Testis;
                                                                                                                                          SEQUENCE OF 24-1019
                                                                                                                                                                                           P,
                                                                                                                                                                                                                        MEDLINE=21175748; PubMed=11279525;
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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                                                                                                                                                                         g P.J., McCarrey J.R., Yang F., Page D
abundance of X-linked genes expressed
. Genet. 27:422-426(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1924735; Stk31.
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7; Conservative
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TNASE-LIKE. POTENTIAL
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ATP (BY SIMILARITY).
7 MW; 1206284ED4E90816 (
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Catarrhini;
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i; Hominidae; Homo.
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                 OF PROTEIN KINASES
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Best Local S
Matches
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083949-----
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UN-2002 (Rel. 41, Last amocration update)
Chaperone protein htpG (Heat shock protein htpG) (High temperature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
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SWART; SM00120; S_TK; 1
SWART; SM00133; TTUOR; 1.
SWART; SM00133; TTUOR; 1.
PROSITE; PS00110; PROTEIN_KIAMSE_ST; FALSE_NEG
PROSITE; PS00110; PROTEIN_KIAMSE_DM; 1.
PROSITE; PS0011; TUDOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000719; Buk_pkiname.
InterPro; IPR0001097; Maternal_tudor.
InterPro; IPR000080; SNase.
InterPro; IPR000290; Suser_thr_pkiname.
InterPro; IPR00299; Tudor.
InterPro; ITR008; Z.
STRAIN=Nichols;
MEDLINE=98332770; PubMed=9665876;
Fraser C.M., Norris S.J., Weinstock G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF285599; AAK31978.1; -.
EMBL; AF332194; AAK17193.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                             protein G).
HTPG OR TP0984.
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                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                             NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          645
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105
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                                                                                                                                                                                                                Spirochaetaceae;
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-> SESS244A380)
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Pred. No. 31;
2; Mismatches
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TNASE-LIKE.
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White O., Sutton G.G.,

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InterPro; ...
InterPro; ...
InterPro; I...
InterPro; I...
InterPro; I...
Pfan; Pro213, HSP09; 2.
A Pfan; Pro213, HSP09; 2.
A Pfan; Pro213, HSP09; 2.
BR PRIME; PRO215, HATTENCK90.
DR SMART; SM00387; HATTENCK90.
DR SMART; SM00387; HATTENCK90.
Chaperone; ATP-binding; Heat shock; Complete proteome.
AFP DOWALN 349 566
DOWALN 349 566
DOWALN 349 566 639
C C SMILARITY).
COOR 40.5; DB 1; Leng'
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ICP4.
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Science 281:375-388(1998).
-!- FUNCTION: Molecular chaperone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dodaon R., Gwinn M., Hickey B.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLood M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Ulterback T., Khalak H., Richardson D., Howell J.K., Chidambaram M., Ulterback T., McDonald L., Artiach P., Bownan C., Cotton M.D., Pylii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                              gene.";
Virology 189:657-667(1992).
                                                                                                                                                                                                                                     MEDLINE=92351564; PubMed=1322594;
Anderson A.S., Francesconi A., Morgan
"Complete nucleotide sequence of the ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses,
Alphaherpesvirinae; Mar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marek's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10388;
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246
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SUBUNIT: Homodimer (By similarity).
SUBURIT: HOMOdimer (By similarity).
SUBCELLULAR LOCATION: Cycoplasmic (By similarity).
SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
PUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLI
OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATIES
OTHER VIRAL GENES, AND AUTORECULATING ITS ON SYMTHESIS. IT IS
REQUIRED FOR THE SWITCH FROM IMMEDIATE-EARLY TO EARLY MODE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WK-RPKSELKEEDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pesvirus (strain GA) (MDHV).
ses, no RNA stage; Herpesviridae;
Marek's disease-like viruses.
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4; Mismatches
                                                                                                                                                                                                                                           organ R.W.;
the Marek's
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Best Local S
Matches
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01-APR-1993
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                             CANDEZ.

Gallus gallus (Chicken).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Chickeryota; Metazoa; Chordata; Craniata; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A4991; EDBEGA.
InterPro; IRPO05205; Herpes ICP4 C.
InterPro; IRPO05205; Herpes ICP4 N.
InterPro; IRPO05206; Herpes ICP4 N.
Pfam; pr0356; Herpes ICP4 C; 1.
Pfam; pr0356; Herpes ICP4 C; 1.
EARTY protein; Transcription regulation; Trans-acting DOMAN M.
15 DOMAN M.
15 DA) 20040 NR; COBGETBEFAD1126 CRC6
EDGERCE 1415 AA; 154936 NR; COBGETBEFAD1126 CRC6
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          PIR; B31872; B31872.
HSSP; P29373; ICBS.
InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000566; Lipocin_cytFABP
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                                                                                                                                                                                                                                                                              KEDLINE-89087453; PubMed=2849937;
Kitamoro T., Momoi T., Momoi M.;
"The presence of a novel cellular retinoic acid-binding protein
chick embryoe: purification and partial characterization.";
Biochem. Biophys. Res. Commun. 157:1302-1308(1988).
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P30370;
                                                                                                                                                                                                                      Biochem.
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUT-1999 (Rel. 36, Last annotation update)
Retinoic acid-binding protein II, cellular (CRABP-II) (Fragment).
                                                                                                                                                                                                                                   Kitamoto T., Momoi
                                                                                                                                                                                                                                                    ERRATUM
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                                                                                                                                                      anoco T., Momoi T., Momoi M.;

chem. Biophys. Res. Commun. 159:371-371(1989).

FUNCTION: CYBADS MAY REGULATE THE ACCESS OF RETINOTC FUNCTION: CYBADS MAY REGULATE THE ACCESS OF RETINOTC ACID TO THE NUCLEAR RETINOTC ACID RECEPTORS.

FUNCTION: CRABP-II MAY PARTICIPATE IN A REGULATORY FEEDBACK MECHANISM TO CONTROL THE ACTION OF RETINOTC ACID ON CELL
                                                                                            TISSUE SPECIFICITY:
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY
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SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELI
PTM. A LONG STRETCH OF SERINE RESIDUES MAY BE
PHOSPHORYLATION.
                                                                                                                        SUBCELLULAR LOCATION: Cytoplasmic.
                                                                               TRANSPORTERS.
                                                                                                                                           DIFFERENTIATION.
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PF00061; lipocalin;
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9; Conserv
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60.0%;
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TO THE FABP/P2/CRBP/CRABP
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Pred. No. 81;
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RESULT 13
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Matches 7; Conserv
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P50568;
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NON TER 36
SEQUENCE 36 AA; 3:
I18B HUMAN STANDARD; P
095998; 096027; 095993; Q9UBR7;
30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                              EMBL; S74933; AAB32580.1; -.
HSSP; P29373; ICBS.
InterPro; IPR000463; Fatty acid BP.
InterPro; IPR000566; LipocIn cytrABP.
Pfam; P70061; Lipocalin; 1.
Pfam; P70061; PROTYACIDBP.
PRANTS; PR00178; PATTYACIDBP.
                                                                                                                                                                                                                                                                                           modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Dikaryota, Metazaa; Chordata, Craniata, Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura, Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last annotation update)
Retinoic acid-binding protein, cellular (CRAB
Kenopus laevis (African clawed frog)
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01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
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ACID TO THE NUCLEAR RETINDIC ACID RECEPTORS.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP
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7; Conserv
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                                                                                                                                                                     AA; 15524 MW;
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34, Last seq
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63.6%;
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Pred. No. 7.3;
0; Mismatches
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Pred. No.
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; 2193DDE7B095EC4A CRC64;
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EMBL; AP110798; AAD17187.1; --
EMBL; AP110798; AAD17189.1; --
EMBL; AP110798; AAD17189.1; --
EMBL; AP110798; AD17190.1; --
EMBL; AP110799; AD17190.1; --
EMBL; AP110801; AD17192.1; --
EMBL; AP110801; AD17192.1; --
EMBL; AP10803; BAN76374.1; --
EMBL; AP122906; AAN41051.1; ALT-
EMBL; AP122906; AAN41051.1; ALT-
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CARBOHYD
                                                                   DOMAIN
DISULFID
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55-58; 61-72; 89-93; 105-142 AND
MEDLINE=99192308; PubMed=10094485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xiang Y., Moss B.; "Identification of human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rubinstein M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND TISSUE SPECIFICITY.
MEDLINE=99146382; PubMed=10023777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, I
15-JUN-2002 (Rel. 41, I
Interleukin-18 binding
                                         CARBOHYD
                                                                                                            SIGNAL
                                                                                                                                                                      MIM,
                                                                                                                                                                                  Genew; HGNC:5987; IL18BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE=99263157; PubMed=10329540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Interleukin-18 binding protein: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novick D., Kim S.-H., Fantuzzi G.,
                                                       CARBOHYD
                                                                                                                                        Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunity 10:127-136(1999)
                                                                                                                          mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUNCTION: Binds to II.18 and inhibits its activity. Funct an inhibitor of the early TII cytokine response. Subscilling ICCATION: Secreted (Potential).

ALTERNATIVE PRODUCTS: 3 ISOPORMS; A/II-18BPA BIL-18BPA BLATERNATIVE SPLICING.

ISBUE (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUB SPECIFICITY: Strongly expressed in heart, lung, pl
                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and spleen.
                                                                                                                                                                      604113;
                                                                                                                                                    IPR003006; Ig_MHC.
           ig; 1.
domain;
 28
197
155
148
148
77
92
101
145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
g protein precursor (IL-
                                                                                                                          Glycoprotein; Signal; Alternative splicing.
           INTERLEUKIN-18 BINDING I
IG-LIKE C2-TYPE DOMAIN.
BY SIMILARITY.
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
                                                                                                                                                                                                ALT_INIT.
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VRSPRRGLQEQEELCFHMWGGKGGLCQSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 29-33; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-68, FUNCTION, ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        novel modulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reznikov L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IL-18BP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the MC51L-53L-54L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B/IL-18BPB AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dinarello C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37-43;
           (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7-43; 46-52;
SPECIFICITY
                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Th1 cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Functions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
SEQUENCE
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB1 outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this extenset is not removed. Usage by and for commercial entities requires a license spreament (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                   Klenk H.-P., Clayton R.A., Tomb J.-P., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Pecerson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., D., Pleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidnan J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.M., D'Andreak R.P., Bowman C., Pujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Arginyl-RNM synthetase (SC 6.1.1.19) (Arginyl-RNM 67 AF0894)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYR ARC
029368;
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                 TIGRFANS; TIGRO0456; argS; 1.
PROSITE; PS00178; AA_TENA_LIGASE I; FALSE_NEG.
Aminoacy1-tRNA synthetase; Protein biosynthesis;
                                                           InterPro, IPR001412; tRNA-synt_I.
Pfam; PF00750; tRNA-synt_1d; 1.
Pfam; PF03485; N-Arg; 1.
PRINTS; PR01038; TRNASYNTHARG.
                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                      Nature 390:364-370(1997).
-i- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP
                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
        Complete proteome.
                                                                                                                                          TIGR; AF0894; -.
                                                                                                                                                     EMBL; AE001042; AAB90346.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaeoglobaceae, Archaeoglobus.
                                                                                                               InterPro;
                                                                                                                           nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBI_TaxID=2234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobalea
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                                                                                                                                                                                                                                                                                  diphosphate + L-arginyl-tena(Arg).
SUBCELLULAR LOCATION: Cycoplasmic
SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARCFU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WVRSPRRGLQEQEEL 181
                                                                                                               IPR001278; Arg_tRNA-synt_1c
IPR005148; N.
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197
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21698
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MISSING (IN ISOFORM B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 11;
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NGTLSLSCVACSRFPNFSILYWLGNGSFIEHLPGRLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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(Arginine--tRNA ligase) (ArgRS)
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                       Ligase; ATP-binding;
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GPT1_CANAL
ID GPT1
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          Search completed: March 26,
Job time : 5.36047 secs
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Query Match
Best Local S
Matches 6
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Best Local Similarity
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15-JUL-1999
15-JUL-1999
15-JUL-1999
                                                                                                                                             TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outeration - the European Bioinformatics Institute. There are content of swiss on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license apresent (See http://www.isb-sib.ch/announce/or send an email to licensesisp-send.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Putative polyamine transporter.
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                                                                                                                                                                                                                                                                                                           TRANSMEN
                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                             Fransport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00324; aa permeases; 1.
PROSITE; PS00218; AMINO_ACID_PERMEASE_1;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002293; AA/rel_prmease1
InterPro; IPR004840; AAc_permease.
InterPro; IPR004841; Permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF080132; AAC31569.1;

    -1- SUBCELLULAR LOCATION: Integral membrane protein (Proba-
-1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a putative polyamine transporter.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McNemar M.D., Gorman J.A., Buckley H.R.; "Isolation and sequence of the GPT1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Candida albicans (Yeast).
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                      1 WKMKPRRNLEEDD
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WYVGPRTNISEED
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                                                                                         Similarity
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(Rel. 38, Last sequence update)
(Rel. 38, Last annotation update)
                                                                       Conservative
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                                                                                      46.5%;
                                                                                                                                               60633 MW;
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Pred. No.
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                                                                     red. No. 35;
Mismatches 4
                                                                                                                                               197DACB76C5FBC9E CRC64;
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                                                                                                        Length 553
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2003, 16:45:03

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Regult
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                      Score
                                                                  40.5
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seq length: 2000000000
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Match Length
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(without alignments)
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2: pir2:*
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T50202
         A.Molecule type: procein
A.Mesidues: 16 CMI2-
A.Mesidues: 16 CMI2-
M.M. Gen Genet: 242, 241-249, 1994
M.J. Gen Genet: 242, 241-249, 1994
A.Mile: The fadD gene of Escherichia coli KI2 is located
A.Meierence number: 341888, MUID:34150456; PMID:8107670
A.McCession: $41590.
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 A; Molecule type: DNA
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pyruvate dehydroge	E83981	N	426	45.3	<u>ب</u>	37
pyruvate denydroge	T86583	N	426	45.6	9	3.7
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probable activator	C85516	N	90	45.3	39	Ğ
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	TIESS	N	1268	46.5	40	G
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hypothetical prote	T01167	N	961	46.5	40	2
hypothetical proce	H83322	N	884	46.5	40	ĭ
•	100001	۲	25.0	.0	ž	č
	BC0361		0	-	>	5

## ALIGNMENTS

#### C. Accession: T50202 R.Barrell, B.G.; Rajandream, M.A.; McDougall, R.C.; Rubantred to the BMBL Data Library, November 1999 A;Reference number: 225045 A;Accession: T50202 A; Map position: A; Experimental source: strain A; Cross-references: A; Molecule type: DNA conserved hypothetical protest pSAC2588.15c [imported] - fission yeast (Schizosaccharomyc C;Species: Schizosaccharomyces poshe C;Date: 09-Umr.2000 #sequence\_revision 09-Umr.2000 #text\_change 09-Umr.2000 A;Residues: 1-237 <BAR> A;Status: preliminary; translated from GB/EMBL/DDBJ Query Match Best Local ! 220 RMKPRRKLRNMDDYL 234 SPDB:SPAC25B8.15c 2 KMKPRRNLEE-DDYL 15 l Similarity 66. EMBL:AL133225; PIDN:CAB61781.1; ce: strain 972h(-); cosmid c25B8 52.9%; ; Score 45.5; ; Pred. No. 4.: 1; Mismatcher Mismatches 멂 2 Ļ McLean, J.; Harris, GSPDB:GN00066; SPDB:SPAC25B8.15c Length 237; Indels 1: Gaps ;;

# R.Zhang, J., Doutscher, M.E. 1988 Nucleic Acids Res. 16, 625-6279, 1988 A;Tile: Escherichia coli RWase D; sequencing of the rnd structural gene and purification A;Telerence number: \$01223; MUID:88289400; PMID:3041371 A;Accession: \$01223 N.Alternate names: ribonuclease D C;Species: Bacherichia coli C;Date: 30-Unn-1991 #sequence revision 30-Unn-1991 #text\_change 01-Mar-2002 C;Accession: S01223; A30431; S41590; D64941; S42849; D21915 A;Cross-references: EMBL:X07055; NID:g42770; FIDN:CAA30098.1; PID:g581215 A;Accession: A30431 A; Residues: 1-375 < ZHA> ribonuclease III (EC 3.1.26.3) rnd - Escherichia coli (strain K-12)

close to rnd at 39.6 min

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C; Accession
R; Hayashi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res 8, 11-22, 2001

NATILLE: Complete genome sequence of enterohemorrhagic Escherichia coli 0157;H7

A;Reference number: A99629; MUID:21156211; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNAse D. processes tRNA precursor (imported) - Escherichia coli (strain 0157:H7, C.Species Escherichia coli (C.Pares 16-Jul-2001 #text_change 03-Aug-2001 C.Pares 16-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C.Pares 16-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001 C.Pares 16-Jul-2001 #text_change 03-Aug-2001
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C;Superfamily: ribonuclease D
C;Keyvords: exonuclease; hydrolase
C;Keyvords: exonuclease D #status experimental <MAT>
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RNase D, processes tRNA precursor [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli
                                             RESULT 4
E85791
                                                                                                                                                                                                                                                                                                                             C; Superfamily: ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:BA000007; PIDN:BAB35936.1; PID:gl3361980; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-375 < HAY>
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A; Residues: 'L', 2-38 < FU2>
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A.Title: The complete genome sequence of Escherichia coli K-12
A.Reference number: A64720; MUID:97426617; PNID:9278503
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A;Experimental source: Strain KI2
R;Blatther, F.R.; Plinkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
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;Accession: A99943
;Hayashi, T.; Wakino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.;
Hayashi, T.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                               Query Match
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Experimental source: strain K-12, substrain MG1655
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nes 7; Conserv
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Local Similarity 63.6%;
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Pred. No. 8.5;
2; Mismatches
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Pred. No. 8.5;
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C;Superfamily: ribonuclease D
hypothetical protein C01F1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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A; Introns: 165/2; 295/3; 478/3
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A;Map position: 2
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A; Residues: 1-532 <STO>
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A;Residues: 1.532 - ROUS
A;Cross references: RMBL:AC004684; NID:g3236234; PID:g3236255
A;Cross references: RMBL:AC004684; NID:g3236234; PID:g3236255
A;Cross references: RMBL:AC004684; NID:g3236234; PID:g3236255
A;Cross references: RMBL:AC004684; N.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, I
euss, D.; Nierman, M.C.; Mitce, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 199
Nature 402, 761-768, 199
A;Fitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Recession: D84796
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N.Alternate names: hypothetical protein Fluv2, 23
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Pates: 05-Mar-1999 Hasquence_revision 05-Mar-1999 #text_change 16-Feb-2001
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A;Experimental source: strain O157:H7, substrain ED1333
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMGL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
A;Reference number: Z14677
                                                                                                           C; Superfamily: Arabidopsis hypothetical protein F13M22.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: T02539
A;Status: translated from GB/EMBL/DDBJ
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Pred. No.
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                       Score 44;
Pred. No.
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L.; Tallon, L.:
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probable heat shock transcription factor - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 Hecquence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T99150
C;Accession: T99150
R;Oliver, K., Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
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A.Residues: 1-112 - COD+
A.Cross-references: EMBL:U58761; NID:gl330391; PID:gl330396; PIDN:AAB00716.1; GSPDB:GNOC
A.Experimental source: strain Bristol NZ; clone COITI
C:Genetics:
                                                                                           C./Accession: AHI764

R.Glaser, P., Frangell, L., Buchrieser, C.; Amend, A., Baquero, F.; Berche, P., Bloecker

R.Glaser, P., Frangell, L., Buchrieser, C.; Amend, A., Baquero, F.; Berche, P., Bloecker

J. Dominguez-Bernal, G.; Duchaud, E., Durand, L.; Dussurget, O.; Entian, K.D.; Fshii, H.

Science 294, 1849-852, 2001

Science 294, 1
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A;Map position: 1
A;Introns: 10/3; 40/3; 67/2; 86/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-539 <OLI>
A;Cross-references: BMBL:Z99168; PIDN:CAB16301.1; GSPDB:GN00066; SPDB:SPAC8C9.14
A;Experimental source: strain 972h-; cosmid c8C9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T15371
                           A;Accession: AH1754
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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A; Accession: T39150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 2
A; Introns: 36/2; 271/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z18338
A; Accession: T15371
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A;Description: The sequence of C. elegans cosmid CO1F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               bacteriophage protein homolog lin2581 [imported] - Listeria innocua (strain Clip11262)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 9; Conserv
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                          RiTheologis A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C. M.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Haizar, L.

Nature 408, 816-820, 2000

A; Authores: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; A; Althores: Hunter, J.R.; Liu, S.X.; Liu, S.X.; Liu, S.X.; Liucs, J.S.; Makii, R.; Mazziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authores: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wh., D.; Yu, G.; Fraser, C.M.; Yenter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Accession: D95652
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A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                               A;Genetics:
A;Gene: T1217.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: D96692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein T1217.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:AL353912; GSPDB:GN00061; ATSP:F3C22.70 A;Experimental source: cultivar Columbia; BAC clone F3C22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Accession: T49020
C.Accession: Masuy, D., Goffeau, A., Boutry, M., Newes, H.W., Rudd, S., Lemcke,
Submitted to the Protein Sequence Database, April 2000
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hypothetical protein p3C22.70 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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A; Residues: 1-384 < PUR>
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                                                                                                                                                                                                                                    A;Cross-references:
                                                                                                                                                                                                                                                                    A; Residues: 1-416 <STO
                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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Best Local Similarity
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    Local Similarity 50. 
les 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
7; Conserv
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                                                                                                                                                                                                                                    GB:AE005173; NID:g11054573;
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                                    50.0%;
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; Score 42; DB
; Pred. No. 31;
3; Mismatches
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Pred. No. 8.6,
3; Mismatches
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Pred. No. 28;
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3.6;
                                                                         DB 2;
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         Indels
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A; Molecule type: DNA

A; Residues: 1-42. HEBNS

A; Cross-references: GH:N7/45; GB:N31542; NID:9143375; PIDN:AAA62683.1; PID:9143379

A; Cross-references: GH:N7/45; GB:N31542; NID:9143375; PIDN:AAA62683.1; PID:9143379

R; KNINSE, F; Ogssawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Broulliet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc

A; Ehrlich, S.D.; Emmerson, P.T.; Entlana, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

A; Authors: Follger, D.; Fritz, C.; Fulita, M.; Fulita, Y.; Fuma, S.; Galizzi, A.; Galler

1ech, J.; Harvood, C.R.; Henaut, A.; Hilbert, M.; Rusita, K.; Lapidue, A.; Lardinois,
A; Mathors: Labber, J.; Lazerevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauseal

Y. M.; Ogsawa, K.; Ogiarza, A.; Oddeya, B.; As, Levine, A.; Liu, H.; Masuda, S.; Mauseal

Y. M.; Ogsawa, K.; Ogiarza, A.; Oddeya, B.; Park, S.H.; Barro, V.; Pohl, T.M.; Porterellic

Rtegor, M.; Rivolta, C.; Roche, B.; Rose, B.; Rose, M.; Sadais, Y.; Sato, T.; Scanton,
A; Mitters, Schleich, S.; Schreeter, R.; Scoffone, P.; Sekigushi, J.; Scotoska, A.; Serous

akwuchi, M.; Tamakoshi, A.; Yamanoto, H.; Yaman, K.; Yasunoon, K.; Yata, K.; Yoshida, K.

A; Mitters, P.; Mighet, A.; Yamanoto, H.; Yaman, K.; Yasunoon, K.; Yata, K.; Yoshida, K.

A; Reference number; A6588; MUD:8844033; PMID:884377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispectes: Bacilius subtils: Cispectes: Bacilius subtils: Cispectes: 12-Apr-1991 #text_change 20-Jun-2000 CiAccession: D36718; B8674 A.; Parvidson, S.; Palva, I. R.Hentilae H.; Palva, A.; Paulin, L.; Arvidson, S.; Palva, I. J. Bacteriol: 172, 5052-5063, Bacilius subtilis: sequence analysis and identity to py: A; Reference number: A36718; MID: 90368588; PMID: 1697875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                         submitted to the Protein S
A;Reference number: Z25013
A;Accession: T49021
                                                                                                                                                                                                C;Accession: T49021
R;Purnelle, B.; Masuy, D.; Goffeau,
                                                                                                                                                                                                                                               hypotherical protein F3C22.80 - Arabidopsis thaliana
hypotherical protein F3C22.80 - Arabidopsis cress)
C. Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: B69674
A;Status: preliminary; nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ફ
   A;Cross-references:
                           A; Molecule type: DNA
A; Residues: 1-451 < PUR>
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                                                                              A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Keywords: acyltransferase; coenzyme A; oxidoreductase;4-77/Domain: lipoyl/biotin-binding homology <LPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology
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EMBL:AL353912; GSPDB:GN00061; ATSP:F3C22.80
                                                                                                                                                                    Sequence Database,
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168
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Pred. No. 33;
3; Mismatches
                                                                                                                                                                                                A.; Boutry, M.; Mewes,
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                                                                                                                                                                    April 2000
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A;Map position: circular
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A;Gene: glrl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-847 < MAR>
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Best Local
Matches
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Similarity
7; Conserv
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   Conservative
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A;Experimental source: C;Genetics:
A;Gene: ATSP:F3C22.80
A;Map position: 3
A;Introns: 4/2; 294/3; 3
A.Molecule type: DNA
A.Molecule 14832 KURD
A.Cross-references: GB:AE009688; PIDN:AAL41169.1; PID:g17738468; GSPDB:GN00186
A.Cross-references: GErain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                           glutamate Mynthase large subunit gitB (imported) - Agrobacterium tumefaciens
C.Spacies. Agrobacterium tumefaciens
C.Spate: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: JC4836
C;Accession: JC4836
R;Margolles-Clark, B.; Saloheimo, M.; Siika-aho, M.; Penttilae,
Gene 17, 171-172, 1996
A;Title: The alpha-glucuronidase-encoding gene of Trichoderma r
A;Reference number: JC4836; MIII:96257277; PMID:8654984
                                                                                                                                                                                                                                                                                           C.Accession: AC2594
R.Wood, D.W.; Getubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.B.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Keywords: glycosidase; hydrolase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-847/Product: alpha-glucuronidase #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Trichoderma reesei
C;Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 17-Mar-1999
                                                                                                                                                                A, Title: The Genome of the Natural Genetic Engineer A, Reference number: AB2577; PMID:11743193
                                                                                                                                                                                                                                                Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z68706; NID:g1419337; EC;Comment: This enzyme releases glucuronic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alpha-glucuronidase (EC 3.2.1.-)
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                                                                                                                                                                                                                                Y.; Biddle, P.; Jung, M.; Krespan,
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Pred. No.
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Pred. No.
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d attached to xylose units
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chromosome

48.8%;

ų. Score 42; Pred. No.

Mismatches

0

Gaps

1.4e+02; DB 2;

Length 1832;

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D97376

hypothetical protein AGR_C_235 [imported] - Agrobacterium tumefaciens (strain C58, Cerec C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: D97376

C;Accession: D97376
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Search completed: March 26, 2003, 16:50:36 Job time: 12.5465 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2332-3238, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A, Reference number: A97359; PMID:11743194
A, Accession: D97376
                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: ACR C_235
A;Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Seatus; preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1856 KUN>
A;Cross-references: GB:AE007869; PIDN:AAK85965.1; PID:g15155024; GSPDB:GN00169
                                                                                                                                                                                                                                              Query Match 48.8%; Score 42; DB 2; Length 1858; Best Local Similarity 53.8%; pred. No. 1.5e+02; Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Searched:
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93
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Ggn2_6/ptodata/1/pinbpas/1958 NRW PBB. pep: *
(Ggn2_6/ptodata/1/pinbpas/PGN NRW PBB. pep: *
(Ggn2_6/ptodata/1/pinbpas/PGN NRW PBB. pep: *
(Ggn2_6/ptodata/1/pinbpas/USO6_NRW PBB. pep: *
(Ggn2_6/ptodata/1/pinbpas/USO6_PRBCOMB. pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIE

No.	Score	Query Match	Query Match Length	DB	ID	Description
_	93	100.0	15	۰	US-10-011-095-21	Sequence 21, Appl
2	93	100.0	15	ø	US-10-010-667A-21	21,
w	93	100.0	267	10	US-09-747-835A-50	Sequence 50, Appl
4,	93	100.0	267	10	US-09-747-835A-51	Sequence 51, Appl
Ņ	93	100.0	339	v	US-10-012-896-879	•
6	93	100.0	339	9	US-09-802-520-11	Sequence 11, Appl
7	93	100.0	339	ø	US-09-895-793-879	879
80	93	100.0	339	ø	US-09-895-814-879	Sequence 879, App
9	93	100.0	339	v	US-10-011-095-2	Sequence 2, Appli
10	93	100.0	339	9	US-10-010-667A-2	Sequence 2, Appli
11	93	100.0	339	10	US-09-759-143-879	Sequence 879, App
12	93	100.0	339	10	US-09-780-669-879	Sequence 879, App
13	93	100.0	339	10	US-09-822-827-879	Sequence 879, App
14	45	48.4	268	5	US-09-854-816-39	Sequence 39, Appl
15	45	48.4	269	10	US-09-854-816-33	Sequence 33, Appl
16	44	47.3	568	10	US-09-815-242-5492	Sequence 5492, Ap
17	44	47.3	568	5	US-09-815-242-12629	Sequence 12629, A
18	43	46.2	147	10	US-09-873-134-2	Sequence 2, Appli
19	43	46.2	351	9	US-10-026-741-47	Sequence 47, Appl

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	1.2
41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	41	42	42	42	42	42	42	42	ť
44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	44.1	45.2	45.2		45.2				4.0
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US-09-725-735A-12	US-10-032-162-17	US-09-886-159-46	US-09-886-149-46	US-09-886-150-46	US-09-886-156-46	US-09-854-816-67	US-09-854-816-37	US-09-854-816-25	US-09-854-816-22	US-09-854-816-21	US-09-854-816-72	US-09-854-816-70	US-09-854-816-14	US-09-854-816-13	US-09-854-816-8	US-09-854-816-73	US-09-476-242-2	US-09-891-609-2	US-09-891-609-4	US-10-007-527A-21	US-09-854-816-71	US-09-854-816-68	US-09-854-816-26	
Sequence 12,	17,	46,	•	46,	6,	67	37	25				70	14	13	Θ,	73	Ņ	Ņ	Sequence 4,	21,	71	Sequence 68,	Sequence 26,	
Appl	App1	App 1	App1	App1	App1	, Appl	App1	Appl	Appl			App1	App1	Appl	Appli	App1	Appli	Appli	Appli	App1	App1	, Appl	App1	

# ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/011,095
CURRENT ILLING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
PRIOR FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PRICED FOR WINDOWS Version 4.0
SEQ ID NO 21 SEQ ID NOS: 32
LENGTH: 15
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Publication No. US20030045682A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel

APPLICANT: Hubert, Rene S.

APPLICANT: Leong, Kahamo, Arthur B.

APPLICANT: Raitamo, Arthur B.
RESULT 2
US-10-010-667A-21
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                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Raitano, Arthur B.
APPLICANT: Asferan Douglas C.
APPLICANT: Micchell, Stave Chappell
TITLE OF INVENTION: ANTHODIES INVINOSEBCIFIC FOR STEAP1 (AS AMENDED)
FILE REFERENCE: 51156200660
                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                            1 WIDIKQFVWYTPPTF 15
1 WIDIKQFVWYTPPTF 15
                                                                                                                                                                                                   15; Conservative
                                                                                                                                                                                                100.0%; Score 93; DB 9; Length 15; 100.0%; Pred. No. 4.5e-08; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                       0
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APPLICANT: Zhang, Jis APPLICANT: Zhang, Jis APPLICANT: Zhang, Jis APPLICANT: Sent, Feliyan APPLICANT: ABUNDAL FELIATING TO G PROTEIN-COUPLED RECEPTOR-LIKE TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE TITLE OF INVENTION: LIKE) POLYEPETIDES AND POLYNUCLEOTIDES FILE REFERENCE: HYS-JOCLP CURRENT TELING DATE: 2000-20-60 PRIOR APPLICATION NUMBER: US 09/747,835A CURRENT FILING DATE: 2000-20-61 PRIOR APPLICATION NUMBER: US 09/653,450 PRIOR APPLICATION NUMBER: US 09/653,450 PRIOR APPLICATION NUMBER: US 09/650,312 PRIOR APPLICATION NUMBER: US 09/650,312 PRIOR APPLICATION NUMBER: US 09/650,42 PRIOR APPLICATION NUMBER: US 09/650,42 PRIOR PRICATION NUMBER: US 09/650,42 PRIOR APPLICATION NUMBER: US 09/650,031 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION NUMBER: US 09/650,042 PRIOR PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PRICATION PR
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PRIOR FILING DATE: 1998-68-30
NUMBER OF SEQ ID NOS: 32
SOPTMARE: PASESEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 15
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APPLICANT: Referan, Douglas C.
APPLICANT: Michail, Steve Chappall
APPLICANT: Michail, Steve Chappall
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: S1158201661
CURRENT APPLICATION NUMBER: US/10/010,667A
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION WIMBER: 05/023,873
PRIOR APPLICATION WIMBER: 05/0323,873
PRIOR APPLICATION WIMBER: 05/067,520
PRIOR APPLICATION WIMBER: 05/067,520
PRIOR APPLICATION WIMBER: 05/067,520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
ID NO 50
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les 15; Conserv
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o. US20020146692A1
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Leong, Kahan
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Wang, Dunrui
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100.0%; Pred. No. 4.5e-08;
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APPLICANT: Zang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Ren, Felyan
APPLICANT: Amend, Vinod
APPLICANT: Amend, Vinod
APPLICANT: Amend, Vinod
TITLE OF INVESTICN: MINISOS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVESTICN: LIKE) POLYPETIDES AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,035A
CURRENT FILING DATE: 2002-03-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/523,450
PRIOR APPLICATION NUMBER: US 09/520,312
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR APPLICATION NUMBER: US 09/598,042
PRIOR PRIING DATE: 2000-07-19
FRIOR APPLICATION NUMBER: US 09/589,042
PRIOR PRIING DATE: 2000-04-25
PRIOR PRIING DATE: 2000-04-25
PRIOR PRIING DATE: 2000-01-21
NUMBER: US 09/489,725
PRIOR PRIING DATE: 2000-01-21
NUMBER: OS 58Q ID NOS: 63
SOSTMARE: Patentin version 3.0
SEG ID NO 51
LENGTH: 267
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US-09-747-835A-50
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; ORGANISM: Homo mapiens
US-09-747-835A-51
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                                                                                                                                                                                                                                                                            US-10-012-896-879
                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                             Sequence 879, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100
Best Local Similarity 100
Matches 15; Conservative
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Best Local Similarity
                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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TYPE: PRT
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211 WIDIKQFVWYTPPTF 225
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Liu, Chenghua
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Wang, Dunrui
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Y. Tom
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100.0%; Pred. No. 8.2e-07;
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Pred. No. 8.2e-07
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APPLICANT: Wantenabe, Yoshihiro
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
ITITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012.896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEG 11 NOS: 1011
SOFTMARE: FASTEQ FOR Windows Version 3.0
SEG 1D NO 879 SEG 10103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lai, Preeti
APPLICANT: Faris, Mary
APPLICANT: Chen; Hesimei
APPLICANT: Chen; Hesimei
APPLICANT: Lion; Craig H.
TITHE OB INVENTION: STEAD-RELATED PROTEIN
FILE REFERENCE: PC-0037 US
FILE REFERENCE: PC-0037 US
CURENT EAPPLICATION NUMBER: US/09/802,520
CURENT FALING DATES: 2001-03-09
NUMBER OF SEQ ID NOS: 11
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                                                                                                                                                                                                                                                                                                                                                      SOPTWARE: PERL Program
SEQ ID NO 11
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                             JS-09-802-520-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%; Pred. No.
Matches 15; Conservative 0; Mismatch
                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                         Matches
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                              277 WIDIKQFVWYTPPTF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WIDIKQFVWYTPPTF 15
                                                                                                                                                         15;
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Vedvick,
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Hepler, William T.
Henderson, Robert A.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                                                                                                                                         Conservative
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ick, Thomas S.
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                                                                                                                                                                           100.0%;
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                                                                                                                                                  Score 93; DB 9;
Pred. No. 1e-06;
Mismatches
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                                                                                                                                                                                                    DB 9; Length 339;
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US-09-895-814-879
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US-09-895-793-879
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TITLE OP INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OP INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21011-544C2
CURRENT APPLICATION NUMBER: US/99/895,793
CURRENT PAPPLICATION NUMBER: US/99/895,793
CURRENT PAPPLICATION NUMBER: US/99/895,793
CURRENT PAPPLICATION NUMBER: US/99/895,793
CURRENT PAPPLICATION DATE: 2001-06-29
SOFTMARE: PRECSEQ FOR WINDOWS Version 3.0
SEQ ID NO 679
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APPLICANT: Dillon, Davin C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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   APPLICANT
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mes 15; Conserv
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Vedvick, Thomas
Carter, Darrick
Li, Samuel X.
                                                                                                                                                                              Day, Craig H. Vedvick, Thomas Carter, Darrick Li, Samuel X.
                                                                                                                                                                                                                                Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Kalos, Michael D.
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Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                   Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
                                                                          Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Kalos, Michael D.
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Hepler, William T.
Henderson, Robert A.
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Stolk, John A.
Day, Craig H.
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o. US20020192763A1
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ilarity 100.0%;
Conservative 0;
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Pred. No. 1e-06;
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Gaps

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APPLICANT: Afer Daniel
APPLICANT: Hobert Rene S.
APPLICANT: Hobert Rene S.
APPLICANT: Leong Kahan
APPLICANT: Raicano, Arthur B.
APPLICANT: Saftran, Douglas C.
APPLICANT: Saftran, Douglas C.
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION. ANTIBODIES IMMUNOSPECIFIC POR STEAPI (AS AMENDED)
PILE REPERBUCE: 51582001610
PILE REPERBUCE: 51582001610
PILE REPERBUCE: 51582001610
PILOR PILLING DATE: DOUGLASSE COURTER APPLICATION NUMBER: 09/323,873
PRIOR HILING DATE: 1999 0-6-10
PRIOR PILLING DATE: 1999 0-6-10
PRIOR APPLICATION NUMBER: 60/087,520
PRIOR PILLING DATE: 1999 0-6-10
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PRIOR PILLING DATE: 1999 
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Sequence 2, Application US/10010667A
Publication No. US2003055217A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
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CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
RUMMER OF SEQ ID NOS: 990
SOFTWARE: FASSESEQ for Windows Version 3.0
SEQ ID NO 879
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Publication No. US20030045682A1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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1 WIDIKQFVWYTPPTF 15

WIDIKQPVWYTPPTF 291

Matches

15;

Mismatches

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Gaps

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APPLICANT: Raitano, ARTHUY B.
APPLICANT: Seffrin, Douglas C.
APPLICANT: METCHAIL SE SWE Chappall
APPLICANT: METCHAIL SE SWE Chappall
APPLICANT: METCHAIL SE SWE CHAPPALL
APPLICANT: METCHAIL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: DAYRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001601
CURRENT APPLICATION UNMERE: 1091.0701.667A
CURRENT FILING DAYE: 1091.0701.206
PRIOR APPLICATION WHERE: 607.007.520
PRIOR APPLICATION WHERE: 607.007.520
PRIOR APPLICATION WHERE: 607.01
PRIOR APPLICATION WHERE: 607.01
PRIOR PILING DAYE: 1998.06-01
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                                                                                              US-09-759-143-879
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 339
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Best Local Similarity
Matches 15; Conserv
                                                Query Match
                                                                                                                                                                                SEQ ID NO 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 879, Application US/09759143 Patent No. US20020022248A1
                           Best Local Similarity
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEG ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.H.
APPLICANT: Skelky, Yasir A.H.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                      LENGTH: 339
TYPE: PRT
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                                                                                                                ORGANISM: Homo sapiens
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                                                                                                                                                                                                         FastSEQ for Windows Version 3.0
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Retter, Marc W.
Stolk, John A.
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Henderson, Robert A.
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Carter, Darrick
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100.0%; Score 93; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Pred. No. 1e-06;
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                              1e-06;
                                                DB 10;
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; ORGANISM: Homo sapiens
US-09-822-827-879
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US-09-780-669-879
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                                                                                                         SEQ ID NO 879
LENGTH: 339
TYPE: PRT
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SEQ ID NO 879
LENGTH: 339
                          Matches
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Patent No. US20020051977A1
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CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MCNeill, Particla D.
APPLICANT: MCNeill, Particla D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                   Local Similarity 100.0%;
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mem 15; Conserv
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1 WIDIKQFVWYTPPTF 15
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Hepler, William
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Retter, Marc W.
Stolk, John A.
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Carter, Darrick
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iilarity 100.0%;
Conservative (
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                                   Score 93; DB 10
Pred. No. 1e-06;
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Pred. No.
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Mismatches
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                                                  DB 10; Length 339;
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Db 277 WIDIKQFVWYTPPTF 291
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RESULT 14
US-09-854-816-39
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                                                                                                                                           Sequence 33, Application US/09854816 Patent No. US20020151473A1 GENERAL INFORMATION:
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APPLICATION NUMBER: US/09/854.816

FILING DATE: 15-May-2001

CLASSIFICATION: «Unknown»

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP. 94080

COMPUTER READABLE FORM:

MEDIUM YYPE: 3.5 inch, 1.44 mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM, PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/965,056
FILING DATE: CUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: Linear SEQUENCE DESCRIPTION: SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P1005R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Constrained Helical Peptides and Methods of
TITLE OF INVENTION: Constrained Helical Peptides and Methods of
                                                                                                APPLICANT: Andrew C. Braisted
J. Kevin Judice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 268 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09854816
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                                       Melissa A.
                                                        Robert S. McDowell
J. Christopher Phelan
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J. Christopher Phelan

 Kevin Judice

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                                       Starovasnik
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Pred. No. 15;
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NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genemtech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STREET: ADDRESSEE: Genemtech)

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COUNTRY: USA

CURRENT COUNTRY: UNDITER: USO/954,816

FILING DATE: CUNLHOWN

RECITANTION INFORMATION:

RECITANTION INFORMATION:

TELEPAX: 650/352-981

INFORMATION FOR SEQ ID NO: 33:

LENGTH: 259 anion acids

TYPE: Anion Acid

TOPOLOGY: Linear

US-09-854-816-33

44.44; Score 45; DB 10; I
                                                                                                          Ouery Match 48.4%; Score 45; DB 10; Length 269;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels
203 WFDITQWLWY 212
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Search completed: March 26, 2003, 17:04:17 Job time : 11.1163 secs

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Post-processing: Minimum Match 0%
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Perfect score:
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Match
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i /cgm2 / prodate/l/iaa/5A COMB.pep;

i /cgm2 / prodate/l/iaa/5A COMB.pep;

i /cgm2 / prodate/l/iaa/5E COMB.pep;

i /cgm2 / prodate/l/iaa/6E COMB.pep;

i /cgm2 / prodate/l/iaa/feTUS COMB.pep;

i /cgm2 / prodate/l/iaa/beckflesi.pep;

i /cgm2 / prodate/l/iaa/beckflesi.pep;
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US-08-965-068-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mode1
Sequence 21, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 33, Appl
Sequence 45, Appl
Sequence 45, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 61, Appl
Sequence 610, Appl
Sequence 62, Appl
Sequence 102, Appl
Sequence 103, Appl
Sequence 104, Appl
Sequence 107, Appl
Sequence 108, Appl
Sequence 109, Appl
Sequence 110, Appl
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APPLICANT: Rene S. Hubert
APPLICANT: Kohan Leong
APPLICANT: Kohan Leong
APPLICANT: Mona S. Gaffran
APPLICANT: Douglas C. Gaffran
APPLICANT: Douglas C. Gaffran
APPLICANT: Douglas C. Gaffran
APPLICANT: Deve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USI.
CURRENT EPPLICATION UNMERE: US/9/323,873A
CURRENT EPPLICATION UNMERE: US/9/323,873A
CURRENT ELING DATE: 1998-06-01
PRIOR APPLICATION UNMERE: 05/091,183
PRIOR APPLICATION UNMERE: 05/091,183
PRIOR PILING DATE: 1998-06-01
PRIOR PILING DATE: 1998-06-01
PRIOR APPLICATION UNMERE: 05/091,183
PRIOR PILING DATE: 1998-06-01
     Sequence 2, Application US/09323873A
Patent No. 632550
PRINTED Daniel B. Afer
APPLICANT: Daniel B. Afer
APPLICANT: Kahn Leong
APPLICANT: Arthur B. Raftano
APPLICANT: Douglas C. Saffran
APPLICANT: Seve Chappell witchell
APPLICANT: Steve Chappell witchell
                                                                                                                                                                          RESULT 2
US-09-323-873A-2
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US-09-323-873A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 32
SOFTWARE: PRSESEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 15
TYPE: PRI

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ilarity 100.0%;
Conservative 0
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US-08-471-70-46
US-08-48-059-46
US-09-48-059-46
US-09-48-070-29
US-09-48-070-28
US-09-144-070-28
US-09-144-070-28
US-09-148-071-28
US-09-149-779-28
US-09-647-719-714-6
US-08-647-714-6
US-08-976-255-10
US-09-976-255-11
US-09-976-255-11
US-09-976-255-11
US-09-976-255-11
US-09-976-255-11
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Pred. No. 2.4e-08;
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Result

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Gaps

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Database

Maximum Minimum Total number Searched:

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Query Match
Best Local Similarity
Matches 6; Conserva
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CURRENT PILLING DATE: 1999-06-01

PRIOR APPLICATION NUMBER: 60/097,520

PRIOR PILLING DATE: 1999-06-01

PRIOR PILLING DATE: 1999-06-01

PRIOR PILLING DATE: 1999-06-01

REGIOR APPLICATION NUMBER: 60/091,183

RIGHT FILLING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 880 ID NOS: 32 NUMBER 05 NUMBER 05 NUM
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MEDIUM TYPE: 3.5 Inch. 1.44 Mb floppy disk
COMPUTER: IRM CC COMPATIBLE
ODERATIOS SYSTEM: PC-DOS/NS-DOS
SOFTWARE: WILDPELIN (Genentech)
APPLICATION NUMBER: US/09/965,556
PLING DATE: 05.46.6271198-1997
CLASSIFICATION NUMBER: US/09/965,556
PLING DATE: 05.46.6271198-1997
ATTORNEY/AGENT NUMBER: 36.700
ARESISTRATION NUMBER: 36.700
REFERRING/DOCKET MUMBER: 36.700
REFERRING/DOCKET MUMBER: 91.005R2
TELEPHONE: 650/202-8674
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LENGTH: 339
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TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tent No.
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                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIILE OF INVENTION: Constrained Helical Peptides and Methods of
IIILE OF INVENTION: Making Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 WIDIKQFVWYTPPTF 291
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STREET: 1 DNA Way
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Robert S. McDowell
J. Christopher Phelan
Melissa A. Starovasnik
James A. Wells
                                        48.4%;
milarity 60.0%;
Conservative
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                                   Score 45; DB 4; Length 268; Pred. No. 11; 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5508384
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45,
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Best Local S
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                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                         APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: POLYMERTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                            STREET:
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US-08-965-056-33
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INFORMATION FOR SEQ ID NO: 33:
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE WillPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION UNMBER: 36,700
REFERENCE/DOCKET NUMBER: P1005R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: James A. Wells
TITLE OF INVENTION: Constrained
TITLE OF INVENTION: Making Same
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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203 WEDITQWLWY 212
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CITY: South San Francisco
STATE: California
                                                                Local Similarity
les 6; Conserv
                                                                                                                                                                          LENGTH: 269 amino acids
TYPE: Amino Acid
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                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/965,056 FILING DATE: 05-No. 6271198-1997 CLASSIFICATION: 530
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                                  1 WIDIKQFVWY 10
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                                                                       Conservative
                                                                                                                                                              Linear
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Robert S. McDowell
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                                                                                      48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.44 Mb floppy disk
                                                                                      Score 45;
Pred. No.
                                                                                                          4
                                                                                                        Length 269
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                                                                       Gaps
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419 Seventh Street, N.W.,

Suite 300

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ODERATING SYSTEM: DC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0, Version #1.25
CURRINT APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-193
PRIOR APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
FILING DATE: 10-SEP-1992
FILING DATE: 10-SEP-1993
FILING DATE: 10-SEP-1993
FILING DATE: 10-SEP-1993
FILING DATE: 10-SEP-1993
FILING DATE: 10-SEP-1993
FILING DATE: 10-SEP-1993
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                                                                                                                                       MEDIUM TYPE: Floppy disk
COMMUTER: IMM PC COMPACIBLE
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
REPLICATION NUMBER: PCT/US93/08528
RAPPLICATION NUMBER: PCT/US93/08528
PRICH APPLICATION DATA: US 07/943,236
APPLICATION NUMBER: US 07/943,236
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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LENGTH: 353 amino acids
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 48.4%; Local Similarity 33.3%; hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Townsend, Kevin G. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56 WVELYNFIWHHPWAF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                         D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York University
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RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348
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Pred. No.
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Query Match
Best Local Similarity
6; Conserva
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  TELEFAX: (703) 836-20
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           NAME: Crane-Feury, Sharon B
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 01753-005
REFERENCE/DOCKET NUMBER: 01753-005
TELECOMPUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FR 91 05392 FILING DATE: 02-MAY-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 12-NOV-
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CITY: Alexandria
STATE: Virginia
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                                                                                                                    TYPE: amino a
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Local Similarity 33.3%;
les 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 31-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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amino acid
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P.O. Box 1404
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                 Conservative
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                            48.4%;
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Pred. No. 15;
5; Mismatches
                 2; Mismatches
                            Score 45; DB
Pred. No. 36;
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                 2; Indels
                                           Length 865;
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               Gaps
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681 WEDITOWLWY 690

1 WIDIKQFVWY 10

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US-08-887-534A-83
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                                                                                                                                                                                                                     RESULT 9
                                                                                                                                                    Sequence 83, Application US/08887534A
Patent No. 6455323
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 60.0%;
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APPLICANT: KIENY, MATIC-Paule
TITLE OF INVENTION: NOVEL HYBRID,
TITLE OF INVENTION: 99160 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          quence 4, Application US/08472240A
tent No. 6284248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
                                                                                                      APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BA
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                                                                                                                   703 WEDITQWLWY 712
                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Protein
LOCATION: 1..854
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TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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ZIP: 22313-1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria
ZIP: 60606
             COUNTRY: United States of America
                                             CITY: Chicago
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                          Illinois
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                                                                                                                          ANTI-BACTERIAL METHODS AND MATERIALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   017753-055
                                                                                                                                                                                                                                                                                                                                  2; Mismatches
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Pred. No. 37;
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TELEFAX: (312) 474-0448
TELEX: (312) 474-6600
INFORMATION FOR SEQ ID NO: 83:
                                                                                                                                                                 ZIP: 20005-3315
COMPUTER READALLS FORM.
MEDIUM TYPE: Ploppy datak
COMPUTEN: THAN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Pacentin Release #1.0, Version #1.30
CURRENT APPLICATION barks.
               APPLICATION NUMBER: PCT/I
PILING DATE: 20-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9-
FILING DATE: 20-OCT-1994
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APPLICATION NUMBER: US/08/887,534A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC computer:
                                                                                                         APPLICATION NUMBER: US/01
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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LENGTH: 403 amino acids
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR TITLE OF INVENTION: SUBTYPE) ANTIGENS
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REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 2841/33996
TELECOMONINICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                      STATE: I
                                                                                                                                                                                                                                                                                                                                           STREET: 1300 I St
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.P. STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 47.3%;
Local Similarity 58.3%;
les 7; Conservative
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                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MONTAGNIER, LUC
DONJON DE SAINT-MARTIN, JACQELINE
COHEN, JAQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLAVEL, FRANCOISE
BORMAN, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUETARD, DENISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HARNEAU, PIERRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                          103
                                  FR 9412554
                                                                                       PCT/FR 95/01391
                                                                                                                                                 US/08/817,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAROLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 4; Length 403;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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RESULT 11
US-08-912-129A-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS (Mindows 95)
OPERATING SYSTEM: MS-DOS (Mindows 95)
SOFTWARE: Microsoft word (ASCII format output)
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION UNDER:
PRIOR APPLICATION UNDER:
PRIOR APPLICATION UNDER:
PRIOR APPLICATION UNDER:
PRIOR APPLICATION UNDER:
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equence 61, Application US/08912129A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.44 ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: DANCKERS, ALGRESS M.
REGISTRATION UNUBER: 32,652
REFERENCE/DOCKET NUMBER: 6109.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-9803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 50.0%;
nes 5; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: RAPID ASSAY FOR SIMULTANEOUS DETECTION AND DIFFERENTIATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 ADDOCT
                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 WIDIKQFVWY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH
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                                                                              847-938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOLDEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NECKLAWS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VALLARI, ANADRUZELA S.
HACKETT, JOHN JR.
HICKMAN, ROBERT K.
VARITEK, VINCENT A. JR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRENNAN,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATHERINE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELIZABETH A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 4; Length 351; Pred. No. 30;
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RESULT 12
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; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-912-129A-61
US-08-817-441-102
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Best Local Similarity 50.0%;
Matches 5; Conservative
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                                                                                  REFERENCE/DOCKET NUMBER: 03260.6005-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
INFORMATION FOR SEQ TO NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 977 smirr secide
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/FF
FILING DATE: 20-0CT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 941
FILING DATE: 20-0CT-1994
PRIOR APPLICATION NUMBER: FR 950
PILING DATE: 03-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 2005-3318
COMPUTER READABLE FORM:
WEDLIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/817,441
FILING DATE: 11-JUL-1997
PRIOR APPLICATION DATA:
                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE TITLE OF INVENTION: SUBTYPE) ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W.
                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                   STRANDEDNESS: single
                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WIDIKOFVWY 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUILLENT, CAROLINE GUETARD, DENISE MONTAGNIER, LUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLAVEL, FRANCOISE
BORMAN, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARNEAU, PIERRE
                               linear
            protein
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; Pred. No. 75;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Length 873
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Query Match Best Local Similarity

46.2%;

Score 43; Pred. No.

DB 4; 75;

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US-08-965-055-68
Sequence 68, Application US/08965056
Patent No. 627118
GENERAL INFORMATION:
APPLICANT: J. Movin Judice
APPLICANT: J. Kovin Judice
APPLICANT: J. Kovin Judice
APPLICANT: J. Christopher Fhelan
APPLICANT: J. Christopher Fhelan
APPLICANT: Melissa A. Scarovasnik
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Similarity
Conserve
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Patent No. 6271198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wilspetin (Genericch)
CURRENT APPLICATION DATA:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timoth)
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Making Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Constrained Helical Peptides and Methods of
                                                                                                                                                                                                                                                                                         202 WFDISKWLWY 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            686 WLDITKWLWY 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 268 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/965,056
FILING DATE: 05-No. 6271198-1997
CLASSIFICATION: 530
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CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                         1 MIDIKQEVWY 10
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                                    James A. Wells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Andrew C. Braisted
J. Kevin Judice
Robert S. McDowell
                                                       Melissa A. Starovasnik
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                   45.24;
  Making Same
                  Constrained Helical Peptides and Methods of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    imothy E.
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                                                                                                                                                                                                                                                                                                                                                                                   Score 42;
Pred. No.
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US-08-965-056-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 71,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 45.2%;
Best Local Similarity 50.0%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 268 amino acids
TYPE: Amino Acid
APPLICATION NUMBER: US/08/955
FILING DATE: 05-No. 6271188-1
CLASSIFICATION: 50-
ATTORNEY/AGENT IMPORMATION:
NAME: TOCCHIA PID. Timochy
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/965,056
FILING DARE: 05-No. 6771189-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, Phb., 7imothy E.
REGISTRATION NUMBER: 56,700
REGISTRATION NUMBER: 56,700
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Winhetin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: J. Kevin Judice
APPLICANT: Robert S. McDowell
APPLICANT: J. Christopher Phelan
APPLICANT: Melissa A. Starovasnik
APPLICANT: James A. Wells
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MEDIUM TIPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: MidTRELIN (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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CITY: South San Francisco
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COUNTRY: USA
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CITY: South San Francisco
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TELEFAX: 650/952-9881
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05-No. 6271198-1997
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                     Timothy E.

 Mismatches

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Pred. No. 32;
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Listing first 45 summaries
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seq length: 2000000000
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3 sp_fungi:
4 sp_human:
5 sp_inverteb
6 sp_manal:
7 sp_mtc:
8 sp_mtc:
10 sp_phage:
10 sp_phage:
11 sp_rodent:
12 sp_vrirus:
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196.889 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	BB	ID	Description
_	91	97.8	338	6	Q9GL50	Q9g150 sus scrofa
2	80	86.0	339	11	Q9CWR7	Q9cwr7 mus musculu
ω	80	86.0	339	F	Q924Z2	Q924z2 mus musculu
4.	80	86.0	339	11	Q924J9	Q924j9 mus musculu
σ.	49	52.7	448	16	Q98CK3	Q98ck3 rhizobium l
6	48	51.6	453	16	Q8UHT8	Q8uht8 agrobacteri
7	46	49.5	122	15	Q9IJL9	Q9ijl9 human immun
89	46	49.5	844	15	Q97002	Q97002 human immun
9	45	48.4	107	N	Q9EVQ0	Q9evq0 escherichia
10	45	48.4	122	15	Q9YXR4	Q9yxr4 human immun
11	45	48.4	122	15	TOXXGD	Q9yxq1 human immun
12	45	48.4	122	15	Q9QIW7	Q9qiw7 human immun
13	45	48.4	122	15	80106O	Q9qiu8 human immun
14	45	48.4	122	15	091LL6	Q9ill6 human immun
15	45	48.4	122	15	Q90DN6	Q90dn6 human immun
16	45	48.4	133	15	Q8URA0	Q8ura0 human immun

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866	865	863	862	862	860	859	858	858	855	854	854	852	852	852	851	850	850	846	841	840	833	833	833	790	358	163	133	133
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012005	Q8Q2X5	012007	012010	012004	Q9E1S7	Q72940	012002	Q87628	Q902H5	012008	092762	Q8UL54	Q8UL55	056567	041641	Q70003	056113	089292	Q9IV31	Q8Q2X4	Q9QKH9	Q9QKI3	Q9QKI4	Q8Q2X3	Q78120	Q90E72	640080	020020
-	Q8q2x5 hur	012007 ch:	_	012004 ch:		Q72940 hur	012002 ch:							056567 hur	O41641 hur	_	O56113 hur		Q9iv31 hur				Q9qki4 hur		_		_	Q8uqz0 hun
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### ALIGNMENTS

RESULT Q9CWR7 ID Q AC Q DT 0	음	O C C C C C C C C C C C C C C C C C C C	RESULT
ILT 2  R7  R87  R9CWR7 PRELIMINARY; PRT; 339 AA.  99CWR7; PRT: 339 AA.  101-UN-2001 (TERMBLrel. 17, Created)  01-UN-2001 (TERMBLrel. 17, Last sequence update)  01-DEC-2001 (TERMBLrel. 19, Last annotation update)	Query Match 97.9%; Score 91; DB 6; Length 338; Best Local Similarity 86.7%; Pred. No. 3.4e-07; Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  1 NIDIKOPTWYTPPTF 15	QSGL50 PRELIMINARY; PRT; 338 AA. QSGL50 PRELIMINARY; PRT; 338 AA. QSGL50 PRELIMINARY; PRT; 338 AA. QSGL50; QSG	LT 1

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A. Arakawa T., Hara A., Pikumishi Y., Konno H., Adachi J., Fikuda S.,
A. Arakawa T., Hara A., Pikumishi Y., Konno H., Adachi J., Fikuda S.,
A. Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A. Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
A. Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T.,
A. Kadota K., Mateud H.A., Ashburnar M., Batalov S., Casawant T.,
A. Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,
A. Fleischmann W., Gasaterland T., Gissi C., King B., Kochiwa H.,
A. Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A. Schriml L.M., Staubli F., Suzuki R., Tonita M., Wagner L., Washio T.,
A. Sakai K., Ocido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A. Blake J., Bolto T., Furuno M., Aono H., Baldarelli R.,
A. Barsh G., Bult C., Fletchner C., Fujita M., Gariboldd M., F.,
A. Mordone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,
A. Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A. Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A. Mourin P., Ring B., Ringwald M., Modriguez I., Sakamoto N.,
A. Suzuki H., Toyo-oka K., Wanga K.H., Weitz C., Whitzaker C., Milning L.,
A. Muynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                            Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; AY029584; AAK50537.1; -. MGD; MGI;1915678; 1010001D01Rik.
                                                                                                                                                                                                                                                                                                                                                                                                "Prostate and non-prostate expression of human STEAP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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Mammalia; Eutheria; Rodentia;
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STEAP OR 2410007B19RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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EMBL; AK010437; BAB26938.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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339 AA; 39264 MW;
MIDIKOFVWYTOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WVDVSQFVWYMPPTF 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V., Manivet
                                                                                                                        Similarity
                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P., Lamblin D.,
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Rodentia;
                                                                                                                                                                                                                                                 39109
                                                                                                                        86.0%;
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19,
21,
                                                                                                                                                                                                                                      MW,
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Last sequence update)
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Pred. No. 2.4e-05;
                                                                                                                        Pred.
                                                                                                                                                         Score 80; DB 11; Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                  Mismatches
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                                                                                                                        2.4e-05;
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Query Match
Best Local Similarity
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Best Local
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Q98CK3;
01-OCT-2001
01-OCT-2001
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01-DEC-2001
01-JUN-2002
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Q924J9;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno S., Sugimoto M., Hochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., Tabata S., Takeuchi C., Yamada M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Tabata S., Sugimoto M., Sugimoto M., Tabata S., Sugimoto M., Sugimoto 
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01-OCT-2001 (TrENBLrel. 18, Last sequence update)
01-OCT-2001 (TrENBLrel. 18, Last senotation update)
01-OCT-2001 (TrENBLrel. 18, Last annotation update)
Alpha-glucosides ABC transporter, substrate-binding
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Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.; 
"Murine six-transmembrane epithelial antigen of the prostate, prostate-
scent cell antigen, and prostate-specific membrane antigen: prostate-
specific cell-surface antigens highly expressed in prostate cancer of 
transgenic adenocarcinoma mouse prostate mice.";
                                                                                                                                                                                                            DNA Res. 7:331-338(2000).
EMBL; AD003005; BAB51618.1; -.
INTERTPTO; IPR000567; SBP bac 1.
Pfam; PF01547; SBP_bacterial_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Mesorhizobium loti)
Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
Phyllobacteriaceae, Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cancer Res. 61:5857-5860(2001).
EMBL, AF297098, AAK83126.1; ...
MGD; MGI:1917608; Steap.
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01-JUN-2002 (TrEMBLrel. 21, Last annocation update)
Six-transmembrane epithelial antigen of the prostate
                                                                                                                                                                              Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome structure 
Wesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MAFF303099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39318 MW;
                                                                                                                                    48920 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.0%;
73.3%;
      52.7%;
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      Score 49;
Pred. No.
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                                                                                                                                          9B7B8569A6945D19 CRC64;
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2.7e-05;
2;
            DB 16;
4.9;
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                                                Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                          symbiotic bacterium
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QSIJL9
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Q9IJL9;
01-OCT-2000
01-OCT-2000
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Chapman P. Clendeming J. Deatherage G., Gillet W., Grant C.,
Kutyawin T., Levy R., Li M. J., McClelland E., Palmieri A.,
Kutyawin T., Lovy R., Li M. J., McClelland E., Palmieri A.,
Kutyawin T., Lovy R., Li M. J., McClelland E., Palmieri A.,
Kutyawin T., Lova B., Seapphimachak C., Jung M., Krespan M., Dordon D.
Zhang S., Yoo H. Tao Y., Jiddle P., Jung M., Krespan M., Dolan M.,
Gordon-Kamm B., Liao J., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J. F., Gordon M.P., Olson M.V.,
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Ol-UNM-2002 (TERMILE) 21. Last sequence update)
Ol-UNM-2002 (TERMILE) 21. Last amocration updat
ABC transporter, substrate binding protein.
AGLE OR ATMOS91 OR AGR_C_1045.
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MEDLINE=21608550; PubMed=11743193;
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Bartoria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8UHT8;
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                                                                     ENV.
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Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                               Envelope glycoprotein (Fragment).
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Almeida N.F. Jr., Woo L.,
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
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Envelope glycoprotein (Fragment).
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InterProv. PRO00138; ENV_GP41.
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Karlsson G., Sodroski J., Morgado M., Galvao-Castro B
von Briseen H., Beddows S., Weber J., Sharp P.M., Sha
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Pfam, PF00517; GP41; 1.
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InterPro; IPR000328; Env_GP41.
InterPro; IPR000777; GP120.
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Wolecular cloning and analysis of functional envelope genes from
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
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STRAIN=HIVBR020.17;
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122 AA;
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Q9EVQ0;
01-MAR-2001
01-MAR-2001
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G9YXR4,
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 19, Last enocation update)
01-MAY-1999 (TrEMBLrel. 19, Last enocation update)
01-MAY-1999 (TrEMBLrel. 19, Last enocation update)
Envelope glycoprotein immunodominant region (Fragment).
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"Structural analysis of phage-borne stx genes and their flanking sequences in shiga toxin-producing escherichia coli and shigelia dyseneriae type 1 strains.";

Infect. Immun. 68:4854-4864 (2000).

ENBL; AJ251452; CAC05542.1;

Hypothetical protein.

SEQUENCE 107 AA; 12177 MW; 8BCD6C52B7D29CE6 CRC64;
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01-MAR-2001 (TERMBLFel. 16, Last sequence update)
01-MAR-2001 (TERMBLFel. 16, Last annotation update)
14-MAR-2001 (TERMBLFel. 16, Last annotation update)
14-MAR-2001 (TERMBLFel. 16, Last annotation update)
15-MAR-2001 (TERMBLFel. 16, Last annotation update)
15-MAR-2001 (TERMBLFel. 16, Last sequence)
15-MAR-2001 (TERMBLFel. 16, Las
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Submitted (NOV-1997) to the EMEL/GenBank/DDBJ databases.
EMBL, AP034039; ARC792911;
InterPro; IRB000338; Env_GP41.
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Costa L.J., Telles J.G.,
Rayfield M.;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-E32511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00517; GP41; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 WCNIKLILWYQSDTF 36
                                                                                                                                                                                   1 WIDIKQFVWY 10
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                                                                                                             AMTMÖLIGAM
                                                                                                                                                                                                                                                         Similarity
6; Conserv
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                    122 AA;
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                                                                                                                                                                                                                                                         Conservative
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                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                    14739 MW; 40D4789EB8C888C2 CRC64;
                                                                                                                                                                                                                                                                                       48.4%;
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Brindeiro R.,
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Pred. No. 5;
2; Mismatches
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                                                                                                                                                                                                                                                                                       Score 45; DB 15; Length 122;
Pred. No. 5.7;
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                                                                                                                                                                                                                                                              Mismatches
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, Schable C., Pieniazek
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Best Local Similarity
Matches 6; Conser
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genotyping and phenotyping analysis of B and non-B Human Immunodeficiency virus type 1 subtypes from patients under HAART."; Submitted (UTL-199) to the EMBL/GenBank/DBJ databases. EMBL, H165537; AAP08482.1; -.. EMBL, H165537; AAP08482.1; -.. InterPro; IPB000328; EMD_GP41.

Fram; P800517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=GP41ERRJ04;
Caride E., Hertogs K., Larder B., I
Caride E., de Sa C.A.M., Eyer W.,
Calazans A.R., Tanuri A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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"HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, ARO34052; AAC79304.1; -.
InterPro, IPR000238; ENV_GP41.
Pfam; PF00517; GP41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TERMELrel 10, Created)
01-MAY-1999 (TERMELrel 10, Last sequence update)
01-MEC-2001 (TERMELrel 19, Last annotation update)
Envelope glycoprotein immunodominant region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tanuri A., Swanson P.A.,
Costa L.J., Telles J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
Viruses, Retroid viruses, Retroviridae, Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane.
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                                                                                                             1 WIDIKOFVWY 10
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                                            WEDITOWLWY 121
                                                                                                                                                                              6; Conserv
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122 AA;
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122 AA; 14792 MW;
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                    14834 MW;
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Brindeiro R., Schable C., Pieniazek D.,
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Last annotation update)
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Pred. No.
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Pred. No. 5.7;
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                                                                                                                                                                                                                                                                                                                                    13711994A52A5B33 CRC64;
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                                                                                                                                                                                                                                                              DB 15;
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L.F.C., Menezes
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01-MAY-2000 (TrEMBLIFE1. 13. Last sequence update)
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4Trom Uganda.";
AIDS Res. Hum. Retroviruses 16:815-819(2000).
EMBL, AF206042; AAP81998.1; -
InterPro; IPB000138; Env_GP41.
Pfam; PF00517, GP41; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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Caride E., Hertogs K., Larder B., D
Machado E., de Sa C.A.M., Eyer W.,
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Downing R., Pieniazek D., Hu D.J., Biryahwaho B., Fridlund C.,
Rayfield M.A., Sempala S.D., Lal R.B.;
"Genetic characterization and phylogenetic analysis of HIV-1 subtype
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                                                                                                                                                                                                                                    Hu D.J., Bagga J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,
Biryahwaho B., Sempala S.D.K., Bayfield M.A., Dondero T.J., Lal R.,
"Similar distribution and continued predominance of HIV-1 subtypes A
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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Search completed: March 26, Job time: 17.6977 secs

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A,Pitic : The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A,Becference number: AB2577; PMID:11743193
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A,Cons-reterences: GB:AE008688; PIDN:AAL41608.1; PID:g17738945; GSPDB:GN00186
A,Experimental source: strain C58 (Dupont)
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R.Wood, D.W., Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, I. Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Go; ster, E.W.
                                                                                                                                                                                                                                        hypothetical protein aglE (imported) - Agrobacterium tumefaciens (strain CSe, C.Species: Agrobacterium tumefaciens C.Species: Agrobacterium tumefaciens C.Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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A, Recession: A97431
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A.; Liu, F.; Wollam, C.; All
Science 294, 2323-2328, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-glucomides-binding periplasmic protein aglE precursor [imported] - Agrobacterium
C.Specles. Agrobacterium tumefacians
C.pate: 30-Sep_2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Map position: circular chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: A97431
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: AGR_C_1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE007869; PIDN:AAK86402.1; PID:g15155534; GSPDB:GN00169
                                                                                                                                                                                                                                                                                     AB2649
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C.; Allinger,
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703
847
847
929
929
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1504
313
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Pred. No.
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S43904
A27224
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G81036
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VCLJSI
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H44001
T09448
S13289
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M.; Doughty, D.;
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                                                                                                                                                              P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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멂 2;

Length 453; Indels

0 Gaps

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M.; McClella

Y.; WOO,

Dupont)

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A; Molecule type: DNA
A; Molecule type: LSS «STEL»
A; Residues : LSS «STEL»
A; Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
A; Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
A; Costaler; H:, Storch-Haggenlocher, B: J Wildemann, B.
A; Title: Distinct populations of human immunodeficiency virus type 1 in l
A; Reference number: S70417; MUID:92144209; PMID:1736940
A; Accession: S70425
                                                                                                                                                                                                                                       A.MoLecule type: DNA
A.Residues: 1-222,'X',224-358 <STE2>
A;Cross-references: EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PID:g60183
C;Superfamily: type B retrovirus env polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein YPO0524 [imported] C/Species: Yersinia pestis
                               AC0065
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A.Description. Distinct populations of HIV-1 in blood and cerebrospinal fluid as A.Reference number; S21990
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Biochem: J. 214, 305-310, 1986
Biochem: Physicochemical and immunochemical characterization of
A;Reference number: A23341; MUID:86242068; PMID:3718469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allergen R7 - perennial ryegrams (tentative sequence) (fragment)
C:Species: Lollum perenne (perennial ryegrams)
C:Date: 05-Jun-1987 #mequence_revimion 05-Jun-1987 #text_change 09-Jun-2000
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Best Local Similarity
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                                                                                                                                        1 WIDIKOFVWY 10
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Pred. No.
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Pred. No. 9.8;
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Pred. No. 0.64;
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                 Yersinia
                                                                                                                                                                                                               Length 358;
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Best Local Similarity
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A; Residues: 1-553 < KUR>
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A; Residues: 1-662 <KLE>
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                                                                    A;Status: preliminary
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Best Local S
Matches 7
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53.8%;
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A.Croser-references: GB:ARD0192; GB:ARD00782; NID:92689415; PIDN:AAB91033.1; PID:92650444
C;Superfamily: acetate-CoA ligase, acetate-CoA ligase homology
F;145-631/Domain: acetate-CoA ligase homology <ACL»
                                                                                                                                                                                                                                                                                                                                                            aceryl-CoA ayrthetaee (acs-1) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jan-2000
C;Dates 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jan-2000
C;Accession: E69274
R;Klenk, H.P., Clayron, R.A., Tomb, J.F., White, O.; Nelson, K.E.; Ketchum, K.A., Dodson, R;Klenk, H.P., Clayron, R.A., Tomb, J.F., White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F.;
; Fieischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
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C;Genetics:
A;Gene: YPOO524
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Pred. No. 19;
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hypothetical membrane spanning protein BMEII0279 [imported] - Brucella melitensis
C.Species Brucella melitensis
C.Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                   Score 44.5; DB 2;
Pred. No. 24;
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R;DelVecChio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, t.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagins, S.; O'Callaghan, D.; Leteser Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A.Title: The genome sequence of the facultative intracellular pathogen Brucella melitenss A;Reference number: AD3252; PMID:11756688 A.Polecule type: DNA A.Polecule type: DNA A.Cross-references: GB:AB0009919; PIDN:AAL53521.1; PID:g17984427; GSPDB:GN00191 A; Experimental source: strain 16M

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Science 294, 849-852, 2001
A.Authores: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, B.; Maitournam, A.; Ma Ok, C.; Schlueter, T.; Simoses, N.; Tierres, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.Title: Comparative genomics of Listeria species, A;Reference number: AB1077, MUID:21537279; PMID:11679669
A;Recession: AH1469
A;Scatus: pre-liminary
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A;Gene: BMEII0279
A;Map position: I
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A; Residues: 1-425 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein Y57G11C.31 - Caenorhabditis elegans (C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C.Accession: T27241
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A;Experimental source: strain Clip11262
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A; Residues: 1-361 <GLA>
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146
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WPEIQOFHWPTPSLY 160
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46.7%; Pred. No. 17;
tive 3; Mismatches
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Pred. No.
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C;Genetics:
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch ma, A.; Mizurani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; in C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 125-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Beference number: A89758; MUID:21311952; PMID:11418146
P-loop protein - Yersinia pestis plasmid pWT1
Clapscies: Yersinia pestis
Clabte: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
Clabte: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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C;Superfamily: GATA-type zinc finger homology C;Superfamily: GATA-type zinc finger C;Keywords: zinc finger conclosy P;932-991/Domain: GATA-type zinc finger homology
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A.Title: White collar-1, a central regulator of blue light responses in Neurospora,

A.;Reference number: 669206, MUID:96203083; PMID:8612589

A.;Accession: 585206
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C:Species: Neurospora crassa
C:Date: 21-Apr-1997 #sequence_revision 09-May-1997 #text_change 11-Jan-2002
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C;Superfamily: acetate-CoA ligase; acetate-CoA ligase homology
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A.Cross-references: GB:BA000018; PID:g13701528; PIDN:BAB42822.1; GSPDB:GN00149
A.Experimental source: strain N315
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C;Accession: A99958
C;Accession: A99958
C;Accession: A99958
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A; Residues: 1-1154 <BAL>
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Best Local Similarity 58.3%;
Matches 7; Conservative
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66.7%; Pred. No. 64

    Mismatches

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Pred. No. 24;
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RESULT 15
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A;Molecule type: DNA
A;Residues: 1-402 <HUD>
A;Cross-references: EMBL:AF053947; NID:g2996286; PID:g2996304; PIDN:AAC13184.1
C;Genetics:
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A.Title: Genomic Cloning and complete sequence analysis of a highly divergent African h
A.Reference number: A53034; MUID:94149849; PMID:8107220
                                                                                                                                                                                                                                                                                                                                                                                                                           gag polyprotein - human immunodeficiency virus type 1 (strain Ant70)
C;Specles: human immunodeficiency virus type 1, HIV-1
C;Specles: O3-May-1994 sequence_revision O3-May-1994 #text_change O7-May-1999
C;Accession: A53034
R;Vanden Haesevelde, M.; Decourt, J.L.; De Leys, R.J.; Vanderborght, B.; van der Groen, J. Virol. 68, 1586-1596, 1994
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Infect. Immun. 66, 5731-5742, 1998
A;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIMS plasmid
A;Reference number; Z18268; MUID:99043898; PMID:9826348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Y1030 - Yersinia pestis plasmid pMT1
C.Spacies: Yersinia pestis
C.Pate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 22-Oct-1999
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C;Superfamily: type E retrovirus
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A;Residues: 1-863 <VAN>
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A; Residues: 1-418 <LIN>
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Best Local
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Best Local :
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:AF074611; NID:g3883003; PID:g3883031; PIDN:AAC82691.1
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Pred. No. 24;
1; Mismatches
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Pred. No. 25;
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Pred. No. 56;
                                                                                                                                                                  Mismatches
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A. Cross references. EMBIL.880000; NID:g510516; PIDN:CAA56323.1; PID:g510517
A.Experimental source; isolate VM.
C. Superiantly. type E retrovirus env polyprotein.
C. Superiantly. type E retrovirus env polyprotein; transmembrane protein C. Keywords. g Jlycoprotein; capsid potesin; coat protein; transmembrane protein F.1-30/Domain. Signal sequence flateaus predicted CPD:
F.1-30/Domain. Examerate flateaus predicted CPD:
F.31-897/Product. coat protein gp41 Hatatus predicted CPD:
F.39-89-736/Domain. Examembrane Hatatus predicted CPD:
F.59-88-139,146,159,184,188,198,230,335,242,263,270,277,292,302,333,345,357,36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     envelope protein precursor - human immunodeficiency virus type 1 (fragment)
C.Species human immunodeficiency virus type 1, HIV-1
C.Date: 10-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C.Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C.Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
C.Dates: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 26-Aug-1999
R.Charmeau, F., Borman, A.M., Quillent, C., Guetard, D., Chamaret, S., Cohen, J., Remy, (
submitted too the SMBL Data Library, UNIV 1994
A.Deportiption: Isolation and envelope sequence of a highly divergent HIV-1 isolate: defir
Search completed: March 26,
Job time : 10.5465 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-877 <CHA>
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Pred. No. 57;
4; Mismatches
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Result
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Maximum Match 100%
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                            and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                   Score
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seq length: 2000000000
Query
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1. | SIIBZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:
2. | SIIBZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:
3. | SIIBZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:
4. | SIIBZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:
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5. | SIIBZ/gogdata/geneseq/geneseqp-embl/AA1981.DAT:
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(c) 1993 - 2003
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片
                 AAY58200
AAB02788
AAY58194
AAU69927
AAM78845
AAM01282
ABG61813
ABB95387
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Compugen Ltd.
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                                                        Human SYRAP-1 pept
Extracellular loop
Human SYRAP-1 prot
Human prostate CDN
Human protein SEQ
P7899 maino acid se
Prostate cancer-as
                                                                                                                                                                                                                                   Description
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### ALIGNMENTS

AAY58200 standard; peptide; 15 AA.

AAY58200;

14-MAR-2000 (first entry)

Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region

Serpentine transmembrane antigen of the prostate; STRAP-1, prostate; transmembrane domain; type IIIa membrane protein; expression; cancer; prostate cancer; hladder anner; colon cancer; pancreatic cancer; coverian; cancer; tumour antigen; simulisation; funce response; cellular; humorral; santiancer vectine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug targetting; recombinant protein.

Synthetic.

domo sapiens.

09-DEC-1999

WO9962941-A2

01-JUN-1998; 30-JUN-1998; 01-JUN-1999; 98US-0087520. 98US-0091183. 99WO-US12157.

(UROG-) UROGENESYS INC. (AFAR/) AFAR D E. (HUBE/) HUBERT R S.

AAE 02780

Human P789P protei six transmen

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RESULT 2
AAE02788
ID AAE0
XX AAE
AC AAE
XC AAE
XX BE
XX BE
XX BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constitution of the structural homology to known human procedure. The STRAP-1 con a significant structural homology to known human procedure. The STRAP-1 con a significant structural commoner PD2. STRAP-1 is thought to be a cype IIIa membrane protein and is expressed predominantly in proseate colls in normal human tissues. Structurally, STRAP-1 is a 139 amino call protein characterised by six transmembrane domains and citeration. On acid protein characterised by six transmembrane domains and citeration. Structurally, STRAP-1 is a 139 amino call protein characterised by six transmembrane domains and citeration contains and citeration protein expression is maintained at high lavels and creation protein expression is maintained at high lavels and creation of the STRAP protein is contained to the structural protein six contains a feature which is shared by certain ion chemnels) or gap-junction protein (from immunohistochemical staining) strap-1 and strap-2 are call-sufface tumour antigens. Immunisation with a STRAP creating induces callular and humoral immunohistochemical staining) strap-1 and strap-2 are call-sufface tumour antigens. Immunisation with a STRAP specific-binding agents, to produce anticancer vaccines and to generate specific-binding agents, to produce anticancer vaccines and to generate specific sinduces of cancers for susceptibility to cancer), as therapeutic and monitoring of cancers for susceptibility to cancer), as therapeutic and monitoring of cancers for susceptibility to cancer), as therapeutic and monitoring of cancers for susceptibility to cancer). STRAP conclusions are specific acids may be used for recombinant protein processing cells for screening inhibitors of STRAP expression state stay of the trapeutic approach is are expressed mainly conditation of STRAP expression. Since high lavels of STRAP conditation of STRAP approaches the specific on price and colline specific on the season of the tissues.
                                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome "p22.3; cancer; prostate; colon; bladder; pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen of the prostate, AAV58194). These peptides were used to raise monoclonal anti-STRAP-1 antibodies. STRAP-1 is the prototype member of the STRAP family of proteins (AAV58194-Y58197) which
                                                                                 Extracellular loop #3 of human STEAP-1, suitable for cloning into
                                                                                                                                                                      AAE02788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      minimal side effects on other tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAY58198-Y58200 represent synthetic peptides that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 22; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOVEL proteins useful as diagnostic markers particularly for prostatic cancer .
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RAITANO A B.
SAFFRAN D C.
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Pred. No.
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AAY58194

AAY58194 standard; Protein; 339 AA

AAY58194;

RESULT 3

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15

1 WIDIKOFVWYTPPTF 15 WIDIKQFVWYTPPTF

Matches

15,

Conservative

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Mismatches

0

Gaps

0

XXXXXXXXXXXXXXXXXXXXXX

Human STRAP-1 protein. 14-MAR-2000

(first entry

Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type IIIa membrane protein; appression; cancer; prostate cancer; bladder cancer; colon cancer; pancreatlo cancer; ovarian cancer; tumour antigen; immunisation; immune response; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; cellular; monitoring; susceptibility; therapeutic inhibitor;

targetting; recombinant

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The present invention relates to human six transmembrane spitbalish antigen of the prostate (SIERAN) protein SIERAN is a member of cell surface serpentine transmembrane sntigens. SIERAN sea as a sea of cell surface serpentine transmembrane sntigens. SIERAN sea used in gene present colon, butched killing only a spread of cancer (e.g. prostate colon, butched killing only a spread strategy of a spread of cancer (e.g. prostate strategy of the spread of cancer (e.g. prostate strategy of the spread of cancer (e.g. prostate strategy of the spread of cancer (e.g. prostate strategy of the spread of cancer (e.g. prostate strategy of the spread of cancer (e.g. prostate strategy) and the spread of cancer (e.g. prostate strategy) and the spread of cancer (e.g. prostate strategy) and the spread of the spread of cancer (e.g. prostate strategy) and the spread of the cancer cells and the spread of spread of the spread of cancer (e.g. prostate) and the spread of spread 
                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins,
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (six transmembrane epithelial antigen of the prostate) expressed in human cancers, useful for detecting and treating
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                                                                                    15 AA;
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100.0%;
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Score 93;
Pred. No.
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4.3e-07;
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                       Length 15;
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This sequence represents a novel human protein, STRAP-1 (serpentine transmembrane antigen of the protected). STRAP-1 is the protectype commber of the STRAP family of proteins (AAYSS19-4YSB197) which can be considered that the protectype considered the strategy of the protein (AAYSS19-4YSB197) which can significant structural homology to known human proteins. The STRAP-1 con significant structural homology to known human proteins thought to be a type IIIa membrane protein and is expressed predominantly in prostate cells in normal human tissues. Structurally, STRAP-1 is a 39 amino cald protein characterised by six transmembrane domains and intracellular N- and C-termini, suggesting that it folds in a construction and two intracellular loops. Can be considered that the strate of the strate of the strate of the strate of cancer. STRAP-1 mRNA and protein expression is maintained at high levels and controlled that an overexpressed in certain other cancers, including bladder, colon, can be considered to the strate proteins is not known. They may be ion channels (from the presence of six transmembrane demains, a feature which is shared by cortain ion channels). STRAP-1 and gap-junction proteins (from immunohistochemical staining). STRAP-1 and
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly for prostatic cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins useful as diagnostic markers
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SAFFRAN D C.
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HUBERT R S.
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98US-0091183.
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AAU69927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CC STRAP-2 are cell-surface tumour antigens. Immunisation with a STRAP CC process induces cellular and humoral immune responses against strapper process of the cellular and humoral immune responses against description of the cellular and humoral immune responses descriptions of the cellular and humoral immune responses against control of the cellular cellular and to generate specific antibodies agains, produce anticancer vaccines and to generate specific antibodies for head antibodies may be used for descendibility to center), as the reposition of the cellular antibodies of the cellular antibodies and the cellular production, as a cellular action may be used for recombinant production, as a cellular action of strapper cellular actions and the cellular action of STRAP conductation of STRAP expression. Since high levels of STRAP conductation and conductation of STRAP expression. Since high levels of STRAP conductation and conductation of STRAP expression. Since high levels of STRAP conductation and conductation of STRAP expression. Since high levels of STRAP conductation and conductation of STRAP expression. Since high levels of STRAP conductation and conductation of STRAP expression. Since high levels of STRAP conductation and conductation of STRAP expression. Since high levels of STRAP conductation of STRAP expression and conductation of STRAP expression.
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09-MAY 2000; 2000US-0588100,
12-MAY 2000; 2000US-0570737,
13-UNA 2000; 2000US-059793,
27-UNA 2000; 2000US-0657813,
10-MUG-2000; 2000US-063215,
29-MUG-2000; 2000US-063216,
06-SER-2000; 2000US-0657279,
02-QCT-2000; 2000US-06851366,
                                                                                                                      WPI; 2001-639232/73.
N-PSDB; AAS64160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cDNA encoded protein #72.
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                                                                                                                                                                     Fanger GR, Rett
Li SX, Wang A,
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                                                                                                                                                                                                            Χu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2001;
                                                                                                                                                                                                                                            (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 WIDIKQFVWYTPPTF 291
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                                                                                                                                                                     Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; cytostatic; immunostimulant; tumour; immunogen
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                                                                                                                                                                                    Harlocker SL, Jimby
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Carter D;
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Claim 2;

Page 549; 579pp; English

The invention relates to isolated prostate-specific

New human prostate-specific polypeptides and polynucleotides useful the diagnosis and treatment of cancer, especially prostate cancer.

for

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Matches
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27-NR-2000; 2000US-9568875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0529325.
01-SEB-2000; 2000US-054936.
15-SEB-2000; 2000US-0643361.
20-QCT-2000; 2000US-0643361.
20-QCT-2000; 2000US-0643325.
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                                                                                                                                                                                                                                                                                                                Tang YT,
Zhao QA,
Xue AJ,
The invention relates to polymuclectides (AAKS1456-AAKS3435) and the encoded polymeptides (AAM78323-AAM80302) that exhibit activity elating to cyrokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                        WPI; 2001-476283/51.
N-PSDB; AAK51978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; mununomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                 Claim 20; Page 3800-3801; 6221pp; English.
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Wang J, Zhang J, Ren F, (
Wejhrman T, Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production of other cytokines in other cell populations. The polymotherides and polymeptides are useful in gene therapy, vaccines or peptide therapy. The polymeptides have various cytokine-like activities, per team cell growth factor activity, hemanonchilatory activity activity, tissue growth factor activity, immunonchilatory activity activity had activity in activity activity and activity activi
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                       were missing at the time of publication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation.
                                           Local Similarity
15,
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Conservative
                                    100.0%;
0
                                           Score 93; DB 22;
Pred. No. 8.4e-06;
       Mismatches
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P789P amino acid sequence
                                         04-OCT-2001
                                                                          AAM01282
                                                                                                              AAM01282 standard; Protein; 339 AA
                                   (first entry
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Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis.

WO200151633-A2

19-JUL-2001.

14-JAN-2000; 2000US-0483672. 16-JAN-2001; 2001WO-US01574.

(CORI-) CORIXA CORP.

Xu J, Dillon DC, Mitcham JL, Kalos MD, Fanger GR, Day CH, A, Meagher MJ; Harlocker SL, Jiang 1 Retter MW, Stolk JA, Y, Reed SG; , Skeiky YAW;

WPI; 2001-425873/45

New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and use in vaccines

Claim 2; Page 510-512; 543pp; English

AMOUTAGE

ANOTAGE

AN The present invention describes polymucleotide sequences (1) which encode prostate specific proteins (II). I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapsutic methods for prostate cancer. They can indicate the level of metastisatis as well as the prostate cancer. They can indicate the level of metastisatis as well as the prostate cancer. They can indicate the level of metastisatis represent polynucleotide and amino acid

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            or the present invention relates to methods of detecting a prostate cancer associated transcript in a cell from a partient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynuclectides (designated PC gense) that content is at least 80 tidentical to them. The prostate cancer-associated polynuclectide sequences to are differentially expressed in prostate thmour tissue or in prostate cancer and are derived from the tissues of various or prostate cancer and are derived from the tissues of various or prostate cancer and mammals. The prostate cancer associated genes are useful for diagnosing or treating prostate cancer, as well as for the streating prostate cancer, as well as for the streating prostate cancer, as well as for the prostate cancer or gents that inhibit prostate cancer. The nucleic said sequences are particularly useful
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16-MAR-2001;
06-APR-2001;
24-APR-2001;
30-APR-2001;
                                                                                                                                                                                                                                                                                                                 Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
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24-JAN-2001;
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  gene therapy, as a vaccine or in antisense applications
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; 2001US-276888P.
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14-JAN-2000) 200003-0438672
27-MAR-2000) 200003-033657
29-MAY-2000) 200003-0568100
12-MAY-2000) 200003-0570737
13-JUN-2000) 200003-0592793
127-JUN-2000) 200003-0592793
127-JUN-2000) 200003-0552727
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10-SEP-2000 200003-0557279
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14-JUL-1998;
23-SEP-1998;
15-JAN-1999;
09-APR-1999;
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FANGER G R.
RETTER M W.
STOLK J A.
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DILLON D C.
MITCHAM J L.
HARLOCKER S 1
  WANG A.
SKEIKY
                                                                      CARTER D.
                                                                                                                                                                                               JIANG Y.
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99US-0439313.
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Pred. No.
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RESULT 9
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Matches
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                                                                                                                                                                                                   03-FEB-2000; 2000US-0496514.
27-APR-2000; 2000US-0560875.
20-7UN-2000; 2000US-0598075.
19-7UL-2000; 2000US-0520325.
01-SEP-2000; 2000US-054936.
15-SEP-2000; 2000US-054936.
15-SEP-2000; 2000US-0549361.
20-00T-2000; 2000US-0583125.
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Fanger GR, Rette
Li SX, Wang A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cencer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer.
                                                                                               Tang YT,
Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccline; peptide therapy; stem cell growth factor; haematopolesis; tiasue growth factor; muntomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human protein SEQ ID NO 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM79829 standard; Protein; 374
Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy -
                                                   WPI; 2001-476283/51.
N-PSDB; AAK52962.
                                                                                                                                                                                                                                                                                                                                                           05-FEB-2001; 2001WO-US04098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                       (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 WIDIKQFVWYTPPTF 29:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                       HYSEQ INC.
                                                                                               Liu C, Drmanac RT, Asundi V, Zhou
Wang D, Wang J, Zhang J, Ren F, (
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 879; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lon DC, Mitcham JL, H
Retter MW, Stolk JA,
ng A, Skeiky YAW, Hep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 93; DE
Pred. No. 8.4
D; Mismatches
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                                                                                                                  C, Cao Y, Wang ZW;
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Carter D;
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Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 350; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE02780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE02780 standard; Protein; 375 AA
                                                                                      Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreatic.
                                                                                                                                                                                                                                                           Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                            Region
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168 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                          302..310
                                                                                                                                                                                                                                                                                              158..166
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Pred. No. 9.2e-06;
Mismatches 0;
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The invention relates to polynucleotides (AAK51456-AAK5145) and the encoded polypeptides (AAM73237-AAM80102) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hasmacropicisis regulating e.g. stem cell growth factor activity, hammomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and of the concert, leukaemia, nervous system disorders, arthritis and 2111 (AAK52582) and 3666 from the sequence listing

Length 374; Indels 0, Gaps 0

Human six transmembrane epithelial antigen of prostate (STEAP)-1 protein.

Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;

Misc-difference 339..340 /label= Immunogenic\_peptide #1
70..91 /label= Transmembrane\_domain #2 /label= Transmembrane\_domain #1 /label= HLA-A2\_binding\_peptide #3 'label= HLA-A2\_binding\_peptide label= HLA-A2\_binding\_peptide #2 "Encoded by TTGTAGAAT" Transmembrane\_domain #5 Transmembrane\_domain #4 HLA-A2\_binding\_peptide #1 Transmembrane\_domain #6 Transmembrane\_domain #3 HLA-A2\_binding\_peptide #5 #4

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Best Local
                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                surface serpentine transmembrane antigens. STEAP-1 gene is located on chromosome 792.2 and is used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate. colon, bladder, kluing ovarian and pencreatic) expressing STEAP or inhibiting growth or Killing cells expressing STEAP in a patient. Comprises administering a vaccine composition to the patient. Treating a patient with a cancer that expresses of STEAP, or inhibiting growth or Killing cells expressing STEAP, comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the variable domains of the heavy and light chains of the monoclonal antibody that specifically binds to STEAP, such that the vector delivers the single chain monoclonal antibody coding sequence to the cancer rells and the encoded single chain monoclonal
                                                                                     Kidney injury associated molecule; kidney injury related molecule; KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                                                                                                                                                                                  AAW86309 standard; Protein; 339 AA.
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                 antibody is expressed intracellularly.
Note: The present sequence is also shown in sequence listing of the specification, but it lacks amino acid residues at its N-terminal e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-1 protein of clone 10. STEAP is a member of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 1A-1B; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-367804/38.
N-PSDB; AAD07067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2001
                                                                                                                                  Kidney injury
                                                                                                                                                         01-MAR-1999
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 22-MAY-1998;
                      26-NOV-1998
                                            WO9853071-A1
                                                                                                                                                                                                                                                        277 WIDIKQFVWYTPPTF 291
                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                             1 WIDIKOFVWYTPPTF 15
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                                                                                                                                                                                                                                                                                                                                             375 AA;
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                       (first entry)
                                                                                                                                  associated molecule HW018 protein.
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   98WO-US10547.
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100.0%; Pred. No.
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Sequence

339 AA;

Local Similarity 1 WIDIKQFVWYTPPTF 15

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Conservative

μ, Score 81; Pred. No. Mismatches

0.00047; ches 2; DB 20;

0, Gaps

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Length 339;

imageable KIM-binding reagent and imaging reagent accumulation

immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; heumatoid arthritis; hyperproliferative disorder; brasst neoplass; cancer; cardiovascular disorder; corneal infection; ocular disorder; corneal infection;

wound healing;

epithelial

cell proliferation; food

Human novel foetal antigen, SEQ ID NO 1456.

Human; foetal tissue antigen; antiinflammatory; neuroprotective;

17-DEC-2001 AAU21212;

(first entry)

AAU21212 standard; Protein;

51

277 WVDISQFVWYMPPTF

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CC by expressing KIM encoding polymucleorides, to pronoce growth and/or control of damaged tissue (e.g. renal tissue), since the KIM proteins care upregulated in injured or regenerating (especially renal) insuses.

CC KIM fusion proteins, conjugates, antibodies and vectors can also be used the temperature of the proteins may be included with an exceptable carrier in pharmaceutical compositions, useful for therapy.

CC prophylaxis of conditions associated with distunction/disregulation or therapy.

CC prophylaxis of conditions associated with distunction/disregulation or proteins, especially renal diseases or impairments of renal CC function in humans (e.g. acute renal failure, acute nephritis). The national function in humans (e.g. acute renal failure, acute nephritis). The conjugated into cella, can disrupt expression of a cellular KIM gene, continued to the product antisense sequences which, when continued the cellular KIM gene, can disrupt expression of a cellular KIM gene, continued to the growth of tumours dependent on CKIM for growth) or compositions. The proteins and polymucleotides are continued to the continued to the continued to the cellular KIM gene, continued to the continued to the continued to the continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, continued to the cellular KIM gene, conti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-1997;
23-MAY-1997;
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0; 2000US-0234274. 0; 2000US-0234997. 0; 2000US-0234998. 0; 2000US-0235484. 0; 2000US-0235834.	0; 2000US-0233064. 0; 2000US-0233065. 0; 2000US-0234223.	0; 2000US-0232401. 0; 2000US-0233063.	0; 2000US-0232399. 0; 2000US-0232400.	0; 2000US-0232397. 0; 2000US-0232398.	0; 2000US-0232081. 0; 2000US-0231968.	0; 2000US-0232080.	0, 2000US-0231413.	0; 2000US-0231243.	0; 2000US-0230438. 0; 2000US-0231242.	0, 2000US-0230437.	0; 2000US-0229509.	0; 2000US-0229345.	0; 2000US-0229343.	0; 2000US-0229287.	0; 2000US-0227009.	0; 2000US-0227182.	0; 2000US-0226681. 0; 2000US-0226868.	0; 2000US-0226279.	0; 2000US-0225758. 0; 2000US-0225759.	0; 2000US-0225757.	0; 2000US-0225270.	0; 2000US-0225268.	0; 2000US-0225266.	0; 2000US-0225214.	0; 2000US-0224519.	0; 2000US-0224518.	0; 2000US-0220963.	0; 2000US-0217496. 0; 2000US-0218290.	200008	20000	200008	20000	200005	20000	20000	2000US-018466			1, 2001WO-US01321.		2-A2.	
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2000; 2000US-0254097. 2001; 2001US-0259678. HUMAN GENOME SCI INC.	; 2000US-0251989. ; 2000US-0251989. ; 2000US-0251990.	; 2000US-0251856. ; 2000US-0251868.	; 2000US-0256719. ; 2000US-0251479.	; 2000US-0251030.	2000US-0250160.	2000US-0249300	2000US-0249297.	2000US-0249264.	2000US-0249244.	2000US-0249218.	2000US-0249216.	2000US-0249215.	; 2000US-0249213.	2000US-0249212.	2000US-0249210.		2000US-0249207.	2000US-0246613.	2000US-0246610.	2000US-0246609.	; 2000US-0246528.	2000US-0246527.	2000US-0246525.			2000US-0246477.	2000US-0246475.	2000US-024461/.	2000US-0241826.	2000US-0241808.		2000US-0	200005	2000US-0239937.	. 2000US-0239935.	2000US-0237039.	2000US-0237038.	2000US-0236802.	2000US-0236370.	200009-0236368.	2000US-0236327.	; 2000US-0235836.

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RESULT 13
AAY22843
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                                                                           16-JUN-1997;
06-NOV-1996;
                                                                                                                                                                                      05-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV, gp41 protein; constrained helical peptide; HIV infection, vaccine; antibody; viral membrane fusion; viral infectivity; ligand affinity purification; protein A replacement; immunoglobulin purification; pottope mimic.
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     (GETH ) GENENTECH INC
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                                                                      97US-0876698.
96US-0743698.
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Pred. No. 7.2;
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The constrained helical peptides are used to treat or prevent HIV creating the specially as vaccines that generate antibodies that prevent viral membrane fusion or infectivity. Vaccines may contain constrained helical peptides derived from several different strains of the prevent that the constrained helical peptides are in affinity purification other uses for the constrained helical peptides are in affinity purification of ilgands (particularly where complete binding protein is not readily contributed to antibody clones from phage display libraries, or as stable or from some time to proceins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of constrained helical peptide(s) by linking side chains on termini of octa:peptide - derived from human immunodeficiency virus gp41 protein, useful in vaccines for treatment and prevention of infection
                                                                                                          16-JUN-1997;
06-NOV-1996;
                                                                                                                                                                                                                                                                                           07-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                  US6271198-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 clade B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; glycoprotein; gp41; antigen; helical conformation; virus-induced membrane fusion; acquired immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Envelope protein gp41 from HIV clade B strain #33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG68314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 180-181; 279pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-286866/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Braisted A,
                                                                                                                                                                                                                         05-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral envelope protein; vaccine; virucide; anti-HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABG68314 standard; Protein; 268 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus
(GETH ) GENENTECH INC
                                                                      16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             202 WEDITONLWY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WIDIKOFVWY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of "floppy" peptides or proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Judice JK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                 97US-049787P.
96US-0743698.
97US-0876698.
                                                                                                                                                                                                                         97US-0965056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 45; DB
Pred. No. 69;
2; Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New cyclic peptides from human immune deficiency virus gp41, useful for treatment or prevention of HIV infection, are constrained to have alpha-helical conformation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Braisted AC,
Wells JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-487624/52
                                                                                                                               16-JUN-1997;
06-NOV-1996;
                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                       HIV, gpd. protein; constrained helical peptide; HIV infection; vaccine antibody; viral membrane fusion, viral infectivity; ligand affinity purification; protein a replacement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO. 33 from WO9820036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY22837;
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                                    Braisted A,
                                                                                                                                                                                           05-NOV-1997;
                                                                                                                                                                                                                                         14-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-1999
                  Wells
                                                                                 (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin purification; epitope mimic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 WFDITQWLWY 211
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                                       Judice JK, McDowell RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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96US-0743698.
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Pred. No. 69;
2; Mismatches
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                                          Phelan JC,
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                                             Starovagnik MA;
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WPI; 1998-286866/25
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production of constrained helical peptide(s) by linking side chains
on termini of octa:peptide - derived from human immunodeficiency
virus gp41 protein, useful in vaccines for treatment and prevention
of infection

Claim 11; Page 174-175; 279pp; English.

(FIV). Specifically. ANYZENO XZENO ANYZENO ANY Peptides AAY22805-Y22917 are derived from Human immunodeficiency virus

X444X4X4444X4X22222222222222222

Sequence 269 AA;

Best Loc Matches Query Match Local Similarity 1 WIDIKOFVWY 10 6, Conservative 48.4%; Score 45; Pred. No. 2 Mismatches 69; 19; Length 269; 2 0 Gaps

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Search completed: March 26, 2003, 16:48:16 Job time : 30.1279 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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O42371 neurospora
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escherichia		MBHM ECOLI	ш	566	40.9	38	
aquifex aeo	067876	HEM2 AQUAE	_	330	40.9	38	_
rhodopseudo		RCEH_RHOVI	_	258	40.9	38	_
escherichia		YEHQ_ECOLI		614	41.4	38.5	•
human immun		ENV_HV1C4	ب	868	41.9	39	۳
human immun		ENV_HV1EL	ш	853	41.9	39	`
escherichia		MDOH_ECOLI	Н	847	41.9	39	٠.
macropus ro		NU4M_MACRO	Н	459	41.9	39	٠.
bacillus ha	_	SERC_BACHD	μ	361	41.9	39	_

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                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Umage by and for commercial smilties requires a license agreement (see http://www.lab-sib.ch/announce/or smid an email to license@abb-sib.ch).
                                                                                                                                                                                                                                                                                                                              -- PUNCTION: PART OF THE BINDING-PROPEN-PEPENDENT TRANSPORT SYSTEM FOR ALPHA-CULOCATIONS SUCH AS SUCGOSE, MALTOSE AND TREHALOSE.
-- SUBCELLULAR LOCATION: Periplasmic (Probable)
-- SIMILARITY; BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING PROTEIN FAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Willis L.B., Walker G.C.;
"A novel Sinochtzobium meliloti operon encodem an alpha-glucosidase
and a periplasmic-binding-protein-dependent transport system for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99328961; PubMed=10400573;
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Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision;
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15-JUN-2002 (Rel. 41, Last amoceation update)
15-JUN-2002 (Rel. 41, Last amoceation update)
15-JUN-2002 (Rel. 41, Last amoceation update)
Alpha-glucosides binding periplasmic protein
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MEDLINE=86218077; PubMed=2423250;
Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Farks R.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Josepha S.F., Gallo R.C., Wong-Staal Parks B.S., Parks W.F., Parks B.S., Parks W.F., Parks B.S., Parks W.F., Parks B.S., Parks W.F., Parks B.S., Parks W.F., Parks B.S.,                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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NCBI_TaxID=11701;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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TRANSPENBARE GLYCOPROTEIN.

BY SIMILARITY.

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1-1- PUNCTION: MAY FUNCTION AS A TRANSCRIPTION PACTOR INVOLVED IN LI-
REGILATION. BINDS AND AFFECTS BLUE LIGHT REGULATION OF THE AL-3
GENE. WCI. AND WCZ PROTEINS INTERACT VIA HOMOLOGOUS PAS DOMAINS,
BIND TO PROMOTERS OF LIGHT REGULATED GENES SUCH AS FRQ, AND
modified and this statement is not removed. Usage by and for commercia: entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@ibb-sib.ch).
                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                            EMBO J.
                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Fungi, Aecomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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                                                                                        ACTIVATE TRANSCRIPTION.
SUBMINIT: HETERODIMEN OF MCI AND WCZ (POTENTIAL).
SUBCELLULAR, LOCATION: Nuclear:
INDUCTION, SP ELUE LUGH.
DOMAIN. THE GUTTAMINE-RICH DOMAIN MIGHT FUNCTION IN ACTIVATING
GENE EXPRESSION.
SIMILARITY: CONTAINS 1 GATA-TYPE ZIMC FINGER.
SIMILARITY: CONTAINS 2 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAINS.
SIMILARITY: CONTAINS 3 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAINS.
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RESULT
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SWART, SM00091; PAG; 3.
SWART, SM00401; ZAF_GATA; 1.
TIGRAPMS; TIGRA00239; sensory_box; 3.
PROSITE; PS00144; GATA, ZN_FINGER 1; 1.
PROSITE; PS00114; GATA, ZN_FINGER 2; 1.
PROSITE; PS0112; PAG; 3.
                                                                                                                Blackshaw S., Snyder S.H.;

"Paraplinopsin, a novel catfish opsin localized to the parapineal organ, defines a new gene family.";

J. Neurosci. 17:8083-8092 (1997).

-1- SUBCELLUIAR LOCATION: Integral membrane protein.

-1- TISSUE SPECIFICITY: PARAPINEAL ORGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                             OPSP
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Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
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Pfam; PF00785; PAC; 2.
Pfam; PF00989; PAS; 3.
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InterPro; IPR000679;
                  This
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BE PHOSEPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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SWISS-PROT entry is copyright. It is produced through a collaboration -
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2; Mismatches
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P46992;
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                         EMBL;
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Obsermaier B., Piravandi E., Rinke M., Domdey H.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
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PRINTS; PR00237; GETRISHODDEN.

PROSITE; PS00237; GE_PROTEIN_RECEP_F1_1;

PROSITE; PS00223; G_PROTEIN_RECEP_F1_2;

PROSITE; PS00223; OPSIN; 1.
                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
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01-FEB-1996 (Rel. 33,
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Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetes.
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                            ; Z49446; CAA89466.1;
S0003707; YJL171C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FIWNTPPLF 166
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BY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 AA.
                                                                                                                             (See http://www.isb-sib.ch/announce/
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(GLCNAC. . .) (E
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                                FUNCTION: INVOLVED IN TRANSLATION TERMINATION.
       ACTIVITY OF ERF1.
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Best Local Similarity
Matches 7; Conserv
MEDLINE=96016209; PubMed=7556078; Stansfield I., Jones K.M., Kushnirov V.V., Dagkesar Poznyakovski A.I., Paushkin S.V., Nierras C.R., Co. Ter-Avanesyan M.D., Tuite M.F.; "The products of the SUP45 (ekF1) and SUP35 genes translation termination in Saccharomyces cerevisian EMBO J. 14.4365-4373[1995].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SUP35 OR SUP2 OR SUP12 OR GST1 OR SAL3 OR PANY2 OR YDR172W OR
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01.NOV-1988 (Rel. 09, Created)
01.NOV-1988 (Rel. 09, Last sequence update)
01.NOV-1988 (Rel. 36, Last annotation update)
                                                                                                                                                                                                 STRAIN=S288C / AB972;
Murphy L., Harris D.E.,
Submitted (NOV-1994) to
                                                                                                                                                                                                                                                                                                                         MEDLINE-88294422; PubMed-2841115;
Kukuchi Y., Shimatake H., Kikuchi A.;
"A yeast gene required for the GI-to-S
containing an A.kinase target site and
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wilson P.G., Culbertson M.R.;
"SUFI2 suppressor protein of yeast.
EF-1 family of elongation factors.",
J. Mol. Biol. 199:559-573(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Localization of possible functional domains
the yeast Saccharomyces cerevisiae.";
FEBS Lett. 215:257-260(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=87219095; PubMed=3556215;
Kushnirov V.V., Ter-Avanesyan M.D., Surguchov A.P., Smirnov V.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINS-88329777; PubMed=3047009;
Kushnirov V.V., Ter-Avanesyan M.D., Telckov M.V.,
Smirnov V.N., Inge-Vechtomov S.G.;
                                                                                                                                                           FUNCTION
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          EMBO J. 7:1175-1182(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE=88172503; PubMed=3280807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                 interact
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                                                                                                                  A.R.,
                                                    to mediate
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BINDS GUANINE NUCLEOTIDES

STIMULATES THE

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SUBUNIT: HETERODIMER OF SUBCELLULAR LOCATION: C SIMILARITY: BELONGS TO ERF3 SUBFAMILY.

HETERODIMER OF TWO SUBUNITS, ONE OF WHICH

Cytoplasmic (Probable).

THE GTP-BINDING ELONGATION FACTOR FAMILY.

BINDS

GTP

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InterPro; IPR004161; EFTU_D2.
InterPro; IPR004795; EF GFP51nd.
Ffam; PP00493; GTP EFTU_D1;
Ffam; PP00443; GTP EFTU_D2; 1.
Pfam; PP03144; GTP_EFTU_D2; 1.
receptors.";
Proc. Natl.;
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                        TIEL MOUSE STANDARD; PRT; 795 AA.

OSEPGI, OSEPHS;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amotation update)
Toll-like receptor 1 precursor (Toll/interleukin-1 receptor-like)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
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EMBL; X07163; CAA30155.1; -.
EMBL; Y00829; CAA68760.1; -.
EMBL; Z46727; CAA6677.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                     SEQUENCE FROM N.A.
STRAIN=BALBC, TISSUE-Macrophage;
MEDLINEZ-2055851, PUDMod-1105740,
OZINSKY A. Underhill D.M., Pontenot J.D.,
Milson C.B., Schroeder L., Aderem A.;
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SGD; S0002579; SUP35.
                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                                                                        immune system is defined by cooperation between Toll-like
                                                                                                The repertoire for pattern recognition of pathogens by the innate
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7; Conserv
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                           Acad.
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                           SC1.
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                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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53.8%;
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SEVERAL SORT OF REFEATS.
CHARGED:
TO ELONGATION FACTORS EF-1.
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
INTERACT MITH GTP/GDP (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
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Pred. No.
                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                           97:13766-13771 (2000)
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                                                                                                                                                    Hajjar A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                    Smith K.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
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Thomson D. P., Campbell C.C., Liew F.Y., Xu D.;
"Clonding of Mus musculus Toll-like receptor 1.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or TLR6 in response to phenol-soluble modulin."; J. Immunol. 166:15-19(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hajjar A.M., O'Mahony D.S., Ozinsky A., Underhill D.M., Aderem A.,
Klebanoff S.J., Wilson C.B.,
"Functional interactions between Toll-like receptor (TLR) 2 and TLR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20571875; PubMed=11123271;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phegosomes.
SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMII
SIMILARITY: CONTAINS 1 TIR DOWAIN.
SIMILARITY: CONTAINS 9 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            response (By similarity).
SUBUNIT: Binds TLR2 via their respective extracellular domains.
Binds MyD88 via their respective TIR domains (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Participates in the innate immune response to micro agents. Cooperates with TLR2 and modulates the response to microbial constituents. Acts via MyD88 and TRAFS, leading to kappa-B activation, cytokine secretion and the inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY. CONTAINS 1 TIR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microbial
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Pfam; PP00560; LER; 8. —
Pfam; PP0163; LERCT; 1.
Pfam; PP01582; TIR; 1.
Pfam; PF00019; LEURICHRPT.
SMART; SM00030; LERCT; 1.
SMART; SM00082; LERCT; 1.
SMART; SM00085; LERCT; 1.
SMART; SM00255; TIR; 1.
            REPEAT
REPEAT
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CARBOHYD
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REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AY009154; AAG37302.1; -.

EMBL; A3316985; AAG35062.1; -.

HSSP; 060603; 1FYW.

MGD; MGI:1341295; Tlr1.
                                                                                            REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                     PROSITE; PS50104; TIR; 1.
Receptor; Immune response; Inflammatory response; Signal;
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001611; LRR.
InterPro; IPR000483; LRR. Cterm.
InterPro; IPR003592; LRR. cut.
InterPro; IPR003591; LRR. typ.
InterPro; IPR003591; TIR. domain.
   CARBOHYD
                                                                                                                                                               TRANSMEM
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                              [ransmembrane;
                                                        Repeat;
                                                                                                                                                                                                           Leucine-rich repeat;
                                 CYTOPLASMIC (POTENTIAL)
LRR 1
LRR 2
LRR 4
LRR 4
LRR 5
LRR 6
LRR 6
LRR 7
LRR 8
LRR 9
TIR 9
N-LINKED
N-LINKED
                                                                                                                                                                                      POTENTIAL.
TOLL-LIKE RECEPTOR 1
                                                                                                                                                               POTENTIAL.
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 (GLCNAC.
(GLCNAC.
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P19550;

01-FEB-1991

01-FEB-1991

15-JUL-1999

Envelope pol
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor (Contains: Exterior membrane
glycoprotein (GP120); Transmembrane 91ycoprotein (GP41)].
ENV.
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Cheng-Mayer C., Outroga M., Tung J.W., Dina D., Levy J.;
"Viral determinants of human immunodeficiency virus type 1 T-cell
"Wiral determinants of human immunodeficiency virus type 1 T-cell
macrophage tropism, cytopathogenicity, and CD4 antigen modulation.
J. Virol. 64:4490-4388(1990).
    CARBOHYD
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Poly;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Burchest Bioinformatics and the EMBL outstation is the Burchest Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M65024; AAA45072.1; -. HIV; M38428; ENV$SF162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; Retroid
NCBI_TaxID=11691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR000777; GP120.
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Pred. No. 33;
3; Mismatches
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last sequence update)
Hypothetical 25-3 kba protein in TIM23-ARE2 in YMR018H OR N3185.
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between the Swiss Institute of Bioinformatics and the EMBL outstati-
the Buropean Bioinformatics Institute. There are no restrictions on
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entities requires a license spreement (See http://www.isb-sib.ch/annou
or send an email to licenseSib-Sh.Ch).
                                       SEQUENCE
                                                                                                                                                                                                       Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces
MCH_TaxID=4932;
                                                  DOMAIN
                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
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                                       196
224 AA;
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3 POTENTIAL.
70 POTENTIAL.
172 POTENTIAL.
172 POLY-GLU.
                                        25344 MW;
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Pred. No. 35;
3; Mismatches
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P71238; P763
01-NOV-1997
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STRAINHRIZ / MG1655;
MEDLINE-97426617; Buthed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland
Blattner F.R., Plunkett G. III, Bloch C.K., Mayhaw G.F.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhaw G.F.
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                      Lipopolysaccharide biosynthesis; Complete proteome.
COMPLICT 108 108 P -> A (IN REP 2)
SEQUENCE 405 AA; 45409 MW; AJD9D91255686043 CRC64;
                                                                                                                                                                                                                                EMBL; U38473; AAC77839.1; -. EMBL; AE000295; AAC75117.1; -.
                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474 (1997)
-I- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF THE SLIME PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
Reeves P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96326333; pubMed=8759852;
Stevenson G., Andrianopoulos K., Hobbs M., Reeves P.R.;
*Organization of the Eacherichia coli K-12 gene cluster responsible
for production of the extracellular polysaccharide colanic acid.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-CCT-2001 (Rel. 40, Last ampleation update)
Putative colanic acid polymerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
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                                                                                                                                                Conservative
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                                                                                                                                                        Score 41; DB
Pred. No. 24;
                                                                                                                                                Mismatches
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Bacteria; Firmicutes;
                                                                                        SubtiList; BG13985; pucK.
InterPro; IR000444; Xan ur permease;
Pfam; PF0086); xan ur permease; 1.
TIGRPAMS; TIGR0801; nne2; 1.
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                                                                                                                                                                                                                                                                                                                    Schultz A.C., Nygaard P.,
                                                                                                                                                                                                                                                                                                                               PubMed=11344136;
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                                                                                                                                    Z99120; CAB15234.1; -.
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97
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 POTENTIAL
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RA KURSE F. OGGESWARE N., MORETE I., Albertini A.M., Alloni G.,
RA ALEVedo V., Bertero M.G., Bessieres P., Boloni A., Borchert S.,
RA Borriss R., Boursier I., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier I., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier I., Brans A., Braun M., Brignell S.C., Bron S.,
RA Broil S.K., Enright M., Royal B., Caphano V., Certer N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Chumings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Britia K.D., Erringon J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Funa S., Galizzi A., Galleron N.,
RA Gdiseppi G., Gly B.J., Haga K., Hahech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holaspel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Gdiseppi G., Gly B.J., Haga K., Hahech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holaspel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Gdiseppi G., Gly B.J., Haga K., Hahech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Halpidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Mesuda S., Mauel C., Medique C.,
RA Wedina N., Wellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA McCha N., Wellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA McCha N., Verlae A., Liu H., Mesuda S., Mauel C., Medique C.,
RA McCha N., Volta C., Rocha B., Roche B., Rose M., Sadale Y.,
RA McCha N., Volta C., Rocha B., Roche B., Rose M., Sadale Y.,
RA McGre D., O'Reilly M., Ogawa K., Ogivaza A., Oudega B., Park S.H.,
RA Parzo V., Pahl T.M., Portecelle D., Porvollik S., Pracedott A.M.,
RA Parzo V., Pahl T.M., Schocke B., Rose M., Sadale Y.,
RA Stelger M., Rivolta C., Rocha B., Schocke B., Rose M., Sadale Y.,
RA Stelger M., Rivolta C., Rocha B., Schocke B., Rose M., Sadale Y.,
RA Stelger M., Tamkoshi A., Tanaka T., Terpatra P., Tognoni A.,
RA Parzo V., Uchtyama S., vandenbil M., Vunnier P., Vassarotti A.,
RA Noseki W., Willey A., Yamanoto Ch., Vannae K., Yassarotti A.,
RA Nocha B., 
                                                                                                                                TICREMMS, TIGROUGUI, 1000.

PROSITE; PSO1116, XANTH_URACIL PERMASE; 1.

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TRANSMEM 18 38 POTENTIAL.

TRANSMEM 43 67 87 POTENTIAL.
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J. Bacteriol. 183:3293-3202(2001).

- EVECTION: UptoANTION: Integral membrane protein (Probable).

- SIMILARTY: BELONGS TO THE XANTHINB/URACII PERMEASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Matches 5
                                                                               InterPro: IPR00896; Hemocyenin.
InterPro: IPR008203; hemocyenin.C.
InterPro: IPR008204; hemocyenin.N.
Pfam; PF00172; hemocyenin, 1.
Pfam; PF03172; hemocyenin, 1.
Pfam; PF03172; hemocyenin. 1.
Pfam; PF03172; hemocyenin.C; 1.
PRINTS; PR01373; hemocyenin.C; 1.
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J. BEDOL. CHEM. 264.19052-19059(1989)

I. EUNCTION: ARYLPHORIN IS A LARVIAL STORAGE PROTEIN (LSB) WHICH SERVY AS A SOURCE OF AROUMEN OF THE SCHEROTIZING SYSTEM OF THE CUTICLE, AND SIA A CORRETE FOR ECVSTERGOID IORNOVAE.

AS A CARRETE FOR ECVSTERGOID IORNOVAE.

I. SUBUNIT: ARYLPHORIN IS A HEXAMER OF SUBUNITS ALPHA AND BETA.

II SUBCELLUMA LOCATION: EXTRACEIDLAR.

ITSSUE SPECIFICITY: FAT BODY.

SIMILARITY: TO ARYB. TO B.MORI STORAGE PROTEINS 1 AND 2, AND ARTHROPOD HEMOCYANINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE=90037032, PubMed=2808410; Willott E., Wang X.-Y., Wells M.A.; Wang X.-Y., Wells M.A.; while the arylphorin, an aromatic "cDNA and gene sequence of Manduca sexta arylphorin, an aromatic amino acid-rich larval serum protein. Homology to arthropod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-104-1990 (Rel. 13, Created)
01-107-1995 (Rel. 12, Last sequence update)
11-007-2001 (Rel. 140, Last simutation update)
Arylphorin bate submit precursor.
Manduca sexts (Tobacco hawkmoth) (Tobacco hormorm)
       PROSITE; PS00209; HEMOCYANIN 1; 1.
PROSITE; PS00210; HEMOCYANIN 2; 1.
Signal; Storage protein; Glycoprotein; Multigene family.
                                                                                                                                                                                                                                                               PIR; B34434; B34434.
HSSP; P04253; 10XY.
                                                                                                                                                                                                                                                                                                                    EMBL; M28395; AAA29304.1; -. EMBL; M28397; AAA29305.1; -.
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Insecta, Pterygota, Neoptera, Endopterygota; Lepidoptera, Glossata,
Ditrysia, Sphingiodea; Sphingidae; Sphinginae; Mandura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARYB_MANSE
P14297;
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Pred. No. 26;
4; Mismatches
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Matches
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Pfam; PF00517; GP41; 1.
AIDS; Coat protein; Polypr
Signal. 29
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01-JUN-1994
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01-UNV-1994 (Rel. 29, Last sequence update)
15-UTL-1999 (Rel. 38, Last sequence update)
Enveloge polyprotein (Psico precursor (Contains: Exterior membrane
glycoprotein (GP10); Transmembrane glycoprotein (GP11)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SMISS-PROT entry is copyright. It is produced through a collabbetween the Swiss Institute of Bioinformatics and the EWBL outst the European Bioinformatics Institute of There are no restrictions use by non-profit institutions as long as its content is in modified and this streement is not removed. Usage by and for com-
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MEDLINE=93021387; PubMed=1404605;
Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M.,
                                                                                            CARBOHYD
                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M93258; -, NOT_ANNOTATED_CDS.
PIR; H44001; H44001.
InterPro; IPR0003777; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http:\vec{l}/www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
Viruses, Retroid viruses; Retroviridae; Lentivirus.
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Pfam; PF00517;
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Huet T., Cheynier R., Meyerhans A., Roelants G.,
"Genetic organization of a chimpanzee lentivirus
Nature 345:356-359(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV). Viruses; Retroid viruses; Retroviridae; Lentivirus. NCBI_TaxID=11723;
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InterPro; IPR000777; GP120.
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Pfam; PF00517; GP41; 1.
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S09990; VCLJSI.
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990 (Rel. 15, Last sequence update)
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polyprotein GB160 precureor [Contains: Exterior membrane
polyprotein GB160 precureor glycoprotein (GP41)].
                                                                                                                               protein;
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score greater than or equal to the score of the result being printed,
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SYJI RAT
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p54576 bacillus su
p77715 caenorhabdi
g97107 schizoscch
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EMBL; AC005053; AAC7950.1; A;
EMBL; AC005059; AAD15620.1; A;
EMBL; AC004969; AAD15620.1; —
EMBL; BC011802; AAH11802.1; —
Genew; HGNC:11378; STEAP
MIN; 604415; —
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GOURBE, O95034;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Six transmembrane epithelial antigen of prostate.
STEAP OR STEAP.
                                                                                                                                                                                                                                     This SNISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Biscinformatics and the EMBL outeration - the ENTOpean Bioinformatics Institute. There are no restrictions on its use ity non-profil finantiations as long. There are no restrictions on its most profile this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to licenses/sib-sib.ch).
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Abu-Threideh J., Stor
Submitted (JUN-1998)
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HEDBELT R.S., Vivanco I., Chen E., Rastegar S., Leong K.,

Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B.,

Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B.,

"STAR: a prostate-specific cell-surfs.H.,

"STAR: a prostate-specific cell-surfs.H.,

Mitchell S.C., Afar D.E.,

"STAR: a prostate tumors.";

"STAR: a prostate tumors.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CIB2 RAT
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DJB7-MOUSE
BIR8-GORGO
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15-JUN-2002 (Rel. 4
Ced-11 protein.
CED-11 OR ZK512.3.
                     GGAB BACSU
P46918,
01-NOV-1995
01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                         1355
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Minor teichoic acids biosynthesis protein ggaB
                                                                                                                                   BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Skidniformatics and the EWBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. House by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensesisb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R. Ainscough R. Anderson K., Baynes C., Berks M., Confeld J., Burton J., Connell M., Copsey T., Coper J., Coulson A., Enfeld J., Burton J., Connell M., Copsey T., Coper J., Coulson A., Craxton M., Dear S., Du Z., Durbin R., Ravello A., Fraser A., Filton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laiseter N., Landelle P., Lightning J., Lloyd C., Mortimore B., O'Callegham M., Patsons J., Perry C., Rifken L., Roppra A., Saundres D., Showheen R., Sins M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Shlaton J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Matson A., Weinstock L., Wilkinson-Sproat J., Walegron R., Wasson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z22177; CAA80145.1; -.
PIR; S40764; S40764.
WormPep; ZK512.3; CE00409.
InterPro; IPR002111; Cat chai
SEQUENCE 1418 AA; 159337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                    15 QVQQNKED---AWIEHDVWRMEI 34
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                                                                                                                                                                                                                         EVAENENDTDNAWTEHDVWAISL 1377
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
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159237 MW; 4FC83B9E7ADF7788 CRC64;
                                                                                                                                                                                                                                                                                                                                 30.5%;
43.5%;
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RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghims S., Galaer P., Goffeau A., Golight Y. S.J., Grandi G.,
RA Ghims S., Galaer P., Goffeau A., Golight Y. S.J., Grandi G.,
RA Ghims S., Glaser P., Goffeau A., Golight Y. S.J., Grandi G.,
RA Ghims S., Glaser P., Goffeau A., Golight Y. S.J., Grandi G.,
RA Ghiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Ghiseppi G., Guy B.J., Haga K., Haiech J., Harwood C., Manno M., Klein C.,
RA Ghiseppi G., Guy B.J., Haga K., Haiech J., Krogh S., Kumano M.,
RA Ghiseppi G., Guy B.J., Haga K., Haiech J., Krogh S., Kumano M.,
RA Ghiseppi G., Guy B.J., Liu H., Masudd S., Kumano M.,
RA Kurita K., Lapidus A., Liu H., Masudd S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masudd S., Mauel C., Nedigue G.,
RA Wedina N., Mellado R.P., Hizuno M., Moseil D., Nakai S., Nobacett A.M.,
RA Woone D., O'Reilly M., O'Gwak K., O'Giwara A., O'ndega B., Park S.H.,
RA Wareno N., Polli T.M., Poutstelle D., Ropwollik S., Presoctt A.M.,
RA Raper M., Rivolta C., Rocha E., Roche B., Rose M., Reynolds S.,
RA Reger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Rapet M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takamaru K.,
RA Yosato V., Uchiyama S., Vandenbol M., Vannier F., Vasasoruti A.,
RA Yosato W., Yoshikawa H.F., Zumetein E., Weller H., Weltzenegger T.,
RA Hinters P., Wijat A., Yamanoto H., Yamane K., Yashwato K., Yata K.,
RA Hinters P., Wijat A., Yamanoto H., Yamane K., Yashwato H.F., Zumetein E., K., Yoshikawa H.F., Zumetein E., K.,
Ra Yoshida K., Yoshikawa H.F., Zumetein E., K., Yoshikawa H., Danchin A.,
Ra Yoshida K., Yoshikawa H.F., Zumetein E., K., Yoshikawa H., Danchin A.,
Ra Yashida K., Yoshikawa H.F., Zumanoto H., Yamanoto H., Yaman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F. Ogsawara N. Moser I. Albertini A.M. Alloni A. Azevedo V. Bertero M.G. Bessieres P. Bolotin A. Borchert S. Borriser K. Berns A. Braun M. Brignell S.C. Bron S. Broulllet S. Bruschl C.V. Caldwell B. Grunno V. Carter N.M. Choi S.K., Codani J.U. Connertool F. Cummings N.J. Demela R.A., Denian K.D., Errigton V., Babet C., Ferrari B., Foulger D., Entland K.D., Errigton V., Fabret C., Ferrari B., Foulger D., Entland K.D., Errigton V. T.
                                                                                                                                                                                                                         Subtiliat; BG11192; 998B.
InterPro; IPPO01173; Glycos transf 2.
Fram, PPO0535; Glycos transf 2; 1.
Transferase; Glycosylitansferase; Complete proteome.
SEQUENCE 900 AA; 107154 MW; PA66459488C2C62F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                    EMBL; U13979; AAA73513.1; -. EMBL; Z99122; CAB15585.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 390:249-256(1997).
-1- FUNCTION: INVOLVED IN THE BIOSYNTHESIS OF GALACTOSAMINE-CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98044033; PubMed=9384377;
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Submitted
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                                                    RSFRHKILTLSSSKVISTHADIWVVNPFFNMEI
                                                                                           RSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                                                                                            Similarity
                                                                                                                                         Conservative
                                                                                                                                                            30.2%;
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                                                                                                                                         8,
                                                                                                                                                               Score 58;
Pred. No.
                                                                                                                                         Mismatches
                                                                                              34
                                                                                                                                                                                 DB 1;
                                                                                                                                         14;
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EMBL

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Gaps

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a collaboration MBL outstation -

outstation

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RESULT 4
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996
01-OCT-1996
15-JUN-2002
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                          sporulation genes.";
Microbiology 142:3103-3111(1996)
                                                                              "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many
                                                                                                                                   Mizuno M., Masuda S.,
Kobayashi Y.,
                                                                                                                                                                                       STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
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P54566;
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Pfam; Pr00089; trypsin; 1.
Hypothetical protein; Plasmid; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE000066; AAB91625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobiaceae;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhizobium sp.
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P55377;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: DISTANTLY RELATED TO PEPTIDASE FAMILY $2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 RRYYRRELFGWEYR-----AKLEPEIWR 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein (Potential).
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630 AA;
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(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
1 protein yqkC.
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RA Actycó V., Bertero M.G., Bessieres P., Bolonia A.,

RA BOTTISER, BOUTSIER I., BESSIERES P., BOLONIA N.,

RA BOTTISER, BOUTSIER I., BOTTISER I., CARDANDO V., CERTER N.M.,

RA BOTTISER, COGASI J.J., COMMETTON I., FOULGET D.,

RA BOTTISER, COGASI J.J., COMMETTON I., COMMINGS N.J., Daniel R.A.,

RA DERLIAN K., DERTINGSON J., FADRET C., FOUNDAM N.J., DANIEL R.A.,

RA DERLIAN K., CALLER P., GOLÍBER Y., FUNBA S., GALIZZI A., GALIZZI A.,

RA GUISESPI G., GGY B.J., HAGRA K., HARECH J., HARVOGU C.R., HENBUR K.,

RA GUISESPI G., GGY B.J., HAGRA K., HARECH J., HARVOGU C.R., HENBUR K.,

RA HILBERT H., HOLSBEPI S., HOSONO S., HALLO N.F., ILAYA M., JONES L.,

RA HOLONIA S., KARAMATA D., KASANATA Y., KLAETT-BLANCHAY M., KLEIN C.,

RA HOLONIA S., LAVINIO S., LANDEN J., NANIE S., NOBACK M.,

RA HOLONIA S., LEVINE A., LATAINOS S., LANDER J., LAZAREVI C.,

RA KURISTA N., HEVINE A., LIU H., MBRUMB S., LANDER J., NOBACK M.,

RA KURISTA N., HEVINE A., LIU H., MBRUMB S., LANDER J., LAZAREVI C.,

RA KOGNE D., O'RELLLY M., O'GAWA K., O'GIVARA A., O'GHEGA B., PEYK S.H.,

RA RATCO V., POHI T.M., POTTERELIE D., POTVOLIK S., PRESOCUT A.M.,

RA PERCO V., POHI T.M., POTTERELIE D., POTVOLIK S., PRESOCUT A.M.,

RA REGGY M., RIVOLE C., ROCHA E., ROCHE B., ROSE M., SEAGLE Y.,

RA SARGY T., SEANARD E., SCHIEST S., SCHOETEER P., TORONIA S.,

RA RIGGY M., TAMASCHI E., NECTE E. P., SIND B. S., SOLOD B.,

RA RIGGY M., RIVOLE C., ROCHA E., ROCHE B., ROSE M., SEAGLE Y.,

RA SARGY T., SEANASH T., TARABI T., TERBARTU K.,

RA SARGY T., SEANASH T., TARABI T., TERBARTU K.,

RA SARGY T., WENDER S., VARDENDE M., WELLE P., TORONIA A.,

RA TAKENDIK B., VARDENCE H., WELLER P., TORONIA A.,

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                                                                    p27775; 0.7665; 0.23512;
01-MG-1992 [Rel. 23 Created]
01-MG-1992 [Rel. 41 Last sequence update)
15-JIN-2002 [Rel. 41 Last amortation update)
Phorbol ester/diacylglycerol-binding protein
uNC-11 0x IX554.2
Caenorhabditis elegans.
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EMBL; Z99116; CAB14297.1; -.
Subtlist; BG11758; yqkC.
Hypothetical protein; Completed Sequence 79 AA; 9287 MW;
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                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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9287 MW; 34852BDAEA
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Pred. No. 1.6;
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"The Caenorthoddis elegans unc.13 gene product is a phospholipid-
dependent high-effinity photol ester receptor.",
Biocham J. 237:995-995(1992)

-- PRINCTION: MAY FORM PART OF A STGNAL TRANSDUCTION BATHWAY,
-- PRANSDUCIG THE SIGNAL FROM DIACYLDICEROL TO EIFFECTOR
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Gardner A.E., Lloyd (
Submitted (MAR-1997)
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MEDLINE-20483775; PubMed-11029047;
MEDLINE-20483775; PubMed-11029047;
Moulder G., Meanyems I.N., Barstead R.J.
"Expression of multiple UNC-13 proceins
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"A phorbol ester/diacylglycerol-binding protein e
gene of Caenorhabditis elegans";
Proc. Natl. Acad. Sci. U.S.A. 88:5729-5733 (1991).
                                                 PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN
                                                                                                                                                                                                                                                                                  WormPep; ZK524.2a; CE15371.

WormPep; ZK54.2b; CE15287.

InterPro; IPR000008; C2.

InterPro; IPR002219; DAG_PE-bind.
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MEDLINE=91288538; PubMed=2062851;
                                                                                                                                                                      Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00168; C2; 3.
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MISCELLANEOUS: MUTATIONS IN UNC-13 CAUSE DIVERSE NERVOUS SYSTEM
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R.J., Rand J.B.;
ins in the Caenorhabditis elegans
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PROSITE; PS000499-C2_DOMAIN 1; 1.

PROSITE; PS50004; C2_DOMAIN 2; 2.

PROSITE; PS500019; DAG PE BIND_DOM 1; 1.

PROSITE; PS500019; DAG PE BIND_DOM 2; 1.

RW Phorbol-ester binding; Zinc; Repeat; Alter:

TDOMAIN 633 742 PHORBOL-ENT.

DOMAIN 693 742 PHORBOL-ENT.

DOMAIN 802 908
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CONFLICT
SEQUENCE
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KEDLINE-97061201; PubMed-8905231;
KAneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura
Kaneko T., Sato S., Kotani H., Tanaka A., Asamoto S., Kimura T.,
Myajima M., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
Chamura S., Shimpo S., Takeuchi C., Mada T., Matanabe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Crested)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
Glycerokinase (EC 2.7.1.30) (ATF:glycerol 36(Glycerokinase) (GK).
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VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium Symechocystis sp. strain PCC8803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synechocystis sp. (strai
Bacteria; Cyanobacteria;
NCBI_TaxID=1148;
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Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                       CAYALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
PATHMAY: Glycerol utilization; rate-limiting step.
SIMILARITY: BELONGS TO THE FUCKINASE / GLUCONOKINASE /
GLYCEROKINASE / XYLULOKINASE PAMILY.
                                                                                                                                                                                                                 FUNCTION:
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i Mismatches
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PÉAM; PF02782; FGGY C; 1.
TIGREAMS; TIGRO1311; 91yo
HSSP; P04191; 1EUL
                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burpean Bioinformatics Institute. There are no restrictions on its Burpean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for convertial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STPAINE-CY. Columbia: WEDLINE-203099; Pubmeda-10907853; WEDLINE-203099; Pubmeda-10907853; Kaneko T., Ratch T., Sato S., Nakamura A., Asamizu E., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Potential calcium-transporting ATPase 13, plasma membrane-type
(EC 3. 6.3.8) (G2+-ATPase, isoform 13).
ACAL3 OR AT3G22910 OR F5N5.8.
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entities requires a license agreement (See
or send an email to license@isb~sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9LIK7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000577; FGGY_kin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YRYKLLNWAYQQVQQNKEDA-WIEHD---VWR 31
                                                                                                                                                                                                                                 ENCYME REGILATION: ACTIVATED BY CALMODULIN (BY SIMILARITY).
SUBCELLULAR LOCATION: Integral membrane protein.
DOWALN: THE N-TERMINUS CONTAINS AN AUTOINHISTORY CALMODULIN-
BINDING DOWALN, WHICH BINDS CALMODULIN IN A CALCIUM-DEPENDENT
PASHION (BY SIMILARITY:
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                           FUNCTION. THIS MAGNESIUM DEPENDENT ENZYME CATALYZES THE HYDROLYSIS OF ATE COUPLED WITH THE TRANSLOCATION OF CALCIUM FROM THE CYTOSOL OUT OF THE CELL OR INTO ORGANELLES (BY SIMILIARITY).

CATALYTIC ACTIVITY: ATP + H(2)O + Ca(2+)(In) = ADP + phosphate +
                                                                                                                                                                                                                                                                                                                                                             Ca (2+) (Out).
                                                                                                                                                                                                                 (E1-E2 ATPASES). SUBFAMILY IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEGNIVGQAYKELTQFYPKAGWVEHDALEIWR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TIGR01311; glycerol kin; 1
PS00933; FGGY KINASES 1; FAI
PS00445; FGGY KINASES 2; 1
                                                                                                                                                                                                7:217-221 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   metabolism; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495 AA; 54351 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                      BAB03036.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71AAC71E76816736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kinase; ATP-binding,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FALSE NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1017 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                          Q9Y705;
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Spindle pole body component alp4.
ALP4 OR SPBC365.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOD RES
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DOMAIN
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PROSITE; PSO1654; ATPAGE E1 E2; Transmembrane; Phosphorylation; Hydrolase; Calcium transport; Transmembrane; Phosphorylation; ATP-binding; Metal-binding; Megnesium; Calmodulin-binding; Multigene family; Hypothetical procein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IRR001757; AfPase B1-E2.
InterPro; IRR001414; Cation_AFPase.
InterPro; IRR001454; Hignase/hydriase.
Pram; PR00152; E1-E2 AfPase; 1.
Pram; PR00689; Cation_AFPase.C; 1.
Pram; PR00689; Cation_AFPase.N; 1.
Pram; PR00689; Jation_AFPase.N; 1.
Pram; PR00689; Jation_AFPase.N; 1.
Pram; PR00689; Jation_AFPase.N; 1.
                                   "The fission yeast gamma-tubulin complex is required is a component of the spindle assembly checkpoint."; EMEO J. 19:6038-6111(2000).
                                                                                                                                                                                                                                 SchizoBaccharomyces pombe (Fission yeast)
Bukaryota; Fungi; Ascomycota; SchizoBaccharomycetes;
SchizoBaccharomycetales; SchizoBaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                    ALP4
                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
  SEQUENCE FROM N.A.
                                                                                                Vardy L.,
                                                                                                                MEDLINE=20532503; PubMed=11080156;
                                                                                                                                      STRAIN=972;
                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                           NCBI_TaxID=4896;
                                                                                                                                                                                                                 Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516
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                                                                                                Toda T
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412
803
822
833
854
874
877
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927
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945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                          AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.6%;
34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CALMODULIN-BINDING (PROBABLE).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2F0265CCE8862916 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                       784
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AN HOOD W. FOAT N. HAYLES J. BEARD D. SOMMAN S.

BY BOOKE K. BOOM D. BOOM S. CHILLINGWORTH T. CHURCHER C.M.

RA BOOKE K. BOOM D. BOOM S. CHILLINGWORTH T. CHURCHER C.M.

RA GERLLES S. GODLE A. HEMIN N. HERTIS D. HIGHED J. Hodges G.

RA GERLLES S. GODLE A. HEMIN N. HERTIS D. HIGHED J. Hodges G.

RA HOLTOY S. HOTHED T. HOWARTH S., HUCKLE B.J. HINT S., Jagels K.

RA HOLTOY S. HOTHED T. HOWARTH S., HUCKLE B.J. HINT S., Jagels K.

RA HOLTOY S. HOTHED T. HOWARTH S., HUCKLE B.J. HINT S., Jagels K.

RA HOLTOY S. HOTHED T. HOWARTH S., HUCKLE B.J. HINT S., Jagels K.

RA HOLTOY S. HOTHED T. HOWARTH S., HUCKLE B.J. HILLER S., GOLLE B.

RA HOLTOY S., O'Nell S., Wangell K., Murphy L. Niblett D., Odell C.,

RA HOOMEY C. O'Nell S., FERTSON D., Quall M.A., Rabbinowitsch E.

RA HOLTOY S. HOMEN S., Saunders D., Seeger K., Sharp S.,

RA KRITHETOTE K., TAYLOT R.G., TIVEY A., MAISH S.V., MATTEN T. WHICHEAS S.,

RA RAN TAYLOT R.G., TIVEY A., MAISH S.V., WATTEN T. WHICHEAS S.,

RA RALLES S., VANESTEEL E., Rieger M., Schnefer M., Mueller-Auer S.,

RA HOLTON S., FRIEZ C., HOLZE E., WOSEL D., HILBERT H.,

RA HOLTON S., FILDS C., HOLZE E., WOSEL D., HILBERT H.,

RA HOLTON S., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA BORZYM K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA BORZYM K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.

RA BORZYM K., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Golfeau A., Cadieu E., Jiener J., Horton S., Aller C., HOLZE K., HUTST S.M.,

RA BORZYM K., Langer J., KANDER Z., HOLTON S., ARTHER S.,

RA GOLFeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottler S.,

RA Golfeau A., Cather M., Mothler H., Benlien J., Petash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                         FXVI.RT STANDARD, PRT; 1574 AA.

062910, 062911, 089092;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UN-2002 (Rel. 4), Last annotation update)
55-UN-2002 (Rel. 4), Last annotation update)
55-UN-2002 (Rel. 4), Last annotation update)
15-UN-2002 (Rel. 4), Last annotation update)
15-UN-2002 (Rel. 4), Last annotation update)
15-UN-2002 (Rel. 4), Last annotation update)
SEQUENCE FROM N.A.
                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                       SYNJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL078627; CAB44767.1; -. EMBL; AB026664; BAA77269.1; -. Microtubules; Mitosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMPL outstation of the Buropean Bioinformatics Institute on Bioinformatics are no restrictions on its use by non-profit institutions as long last is content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                592 FRYFLL---LRHVEMQLENSWVQHSKNSAWRL 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 YRYKLINWAYQQVQQNKEDAWIEH---DVWRM 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE GCP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANIZING CENTER (MTOC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
   (ISOFORMS 1 AND
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Pred. No.
                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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TO THE INOSITOL-1,4,5

EMBL; U45479; AAB60525.1; -.
EMBL; U45479; AAB60526.1; -.
EMBL; AJ006855; CAA07267.1;
InterPro; IPR005135; Exo\_end

IPR005135; Exo\_endo\_phos.

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"Tissue-specific alternative splicing generates two synaptojanin
laoforms with differential membrane binding properties.";
J. Biol. Chem. 2712486-2486(1998).
-i- FUNCTION: INOSITOL 5-PHOSPHATASE WHICH HAS A ROLE IN CLATHRIN-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTERNATIVE SPLICING.
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Woscholski R., Finan P.M., Radley E., Parker P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96394655; PubMed=8798761;
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                                                                                                                                                                                                                                                                                                                                                         DOWAIN: THE C-TERMINAL PROLING-RICH REGION MEDIATES BINDING TO A VARIETY OF SHE DOWAIN-CONTAINING PROTEINS INCLUDING MEMPHIPHYSIN, SHIP4, SHEPS, SHEPS, AND GRB2.

SHIP4, SHEPS, SHEPS, AND GRB2.

CHIVITY OF THE CATALYTIC DOWAIN DOES NOT ALTER THE CATALYTIC FORTH THE SHEP CONTAINS ACT DOWAIN DOES NOT ALTER THE CATALYTIC SHIPLARITY: IN THE CRIVINAL SECTION, BELONGS TO THE INOSITOL-1,4,5, TRIEDHOGSHATE S-PHOSPHANSE PAMILY.

SHALARITY: CONTAINS I SAC DOWAIN: OMOTIF (RRM).
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CATALYTIC ACTIVITY: D-myo-inositol 1,4,5-trisphosphate + H(2)O = D-myo-inositol 1,4-b-gblosphate + phosphate.

SUBCELLULAR LOCATION: LOCALIZED MAINLY IN THE SOLUBLE FRACTION (BY
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Best Local
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OSUPN3; OSUKD0; OSULO3; OSUSA3;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Actin cross-linking family protein 7 (Macrophin)
(620 kba actin-binding protein) (ABP620).
ACF7 OR ABP620 OR KIANA0465 OR KIANA1251.
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                                                                                                                                                                                                                MEDLINE-20001959, PubMed=10529403;
Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N.,
Takahashi M., Ishigaki T., Hamaguchi M.;
Twolecular cloning of macrophin, a human homologue of Drosophila
Nakapo with a close structural similarity to plectin and dystrophin.";
Biochem. Biophys. Res. Commun. 264:568-574(1999).
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Pfam; PF03372; Exo_endo_phos; 1.
SMART; SM00128; IPPc; 1.
                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=20026884; PubMed=10559237;
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                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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PROSITE; PS50275; SAC; 1.
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InterPro;
                  MEDLINE=20039619; PubMed=10574462;
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Ishikawa K.-I., Kikuno R.,
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(IN REF. 2)
  Hirosawa M., Nomura N.,
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    Pfam, PP00143; spectrin; 36.
Pfam, PP0187; GAS2, 1.
Probom, PP0187; GAS2, 1.
SHART, SH000013; GH; 2.
SHART, SH00064; EFh; 2.
SHART, SH0023; GAS2, 1.
SHART, SH00123; GAS2, 1.
SHART, SH00123; GAS2, 1.
SHART, SH001213; GAS2, 1.
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*Prediction of the coding sequences
The complete sequences of 100 new of
for large proteins in vitro.";
DNA Res. 6:337-345(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98116662; PubMed=9455484;
Seki N., Ohira M., Nagase T., Ish
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TISSUS SPECIFICITY: UDUITOUSLY EXPRESSED.
SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 3 SPECIFIX REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J AB029290, BAAB3821.1; -. AB029290, BAAB3821.1; -. AB029290, BAAB6565.1; -. AB033077; BAAB6565.1; -. AB03020.1; -. AB007934; BAA32310.1; -.
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; Q01082; 1E
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                                                                                                                                               PS50021; CH; 2.
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PS50002; SH3; FALSE
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PS00020; ACTININ_2;
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Kumano S., Manter D., M
Brown A.E., Jackson P.J
         EMBL; AP001118; BAB12944.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gymbiotic bacterium).
Bacteria; Proteobacteria;
NCBI_TaxID=118099;
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16-OCT-2001
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
2,3,4,5-terthydropyidine-2-caboxylate N-succinyltransferas
(RC 2.3,117) (Terrahydrodipicolinate N-succinyltransferase)
(THP succinyltransferase) (Tetrahydropicolinate succinylase).
DAPD OR BUZ29.
This SHISS-PROT entry is copyright. It is produced through a collaboration between twiss Institute of Bibbinformatics and the SMBL outstation - the European Bibinformatics Institute. On the stropean Bibinformatics Institute. On the use by non-profit institutions as long as its content is along wolffied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.iab-sib.ch/announce/or send an enail to licenses@ib-sib.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF188935; AAF13609.1; -. Hypothetical protein; Plasmid. SEQUENCE 95 AA; 11613 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=106490 1998;
MEDLINB=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori
Shigenobu S., Watanabe H., Hattori
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
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artinez Y., Svensson R., Tatum L.R.,
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                                                                                                                                                                                                                                                                                                                                        MEDITINE=6337999; Publichede6680807), Zhou L., Fleischmann R.D., White O., Olsen G.J., Zhou L., Fleischmann R.D., Sutton G.G., Blake J.A., FizzGerald L.M., Clayton R.A., Godayne J.D., Stein G.G., Blake J.A., FizzGerald L.M., Clayton R.A., Godayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Fhhrmann J.L., Nguyen D., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.M., Hanna M.C., Corton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Bordovsky M., Klenk H.-P., Fraser C.M., Smith H.O., Weese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGREPAMS; TIGRO0965; ÓADD, 1
PROSITE; PRODIOJ; HEXABEP TRANSFERASES; 1.
PROSITE; PRODIOJ; HEXABEP TRANSFERASES; 1.
Transferase; Acyl-transferase; Repeat; Dyroteome.
Diaminopimolare biosynthesis; Complete proteome.
SEQUENCE 274 AA; 31144 MM; ESEZIEES564A936 CRC64;
                                                                                                                                                                                                This SWISG-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation - the Buropean Bioinformatics Institute on There are no restrictions on its use in mon-profit institutions as long as its content to in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P56220; 3TDT.
InterPro; IPR001451; Hexapep_transf.
Pfam; PF00132; hexapep; 5.
                                                                                                                                                                EMBL; U67568; AAB99279.1; -. TIGR; MJ1273; -.
                                                                                                                                                                                                                                                                                                                      Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q58669;
                                                                                                     ProDom; PD011688; DUF43; 1.
Hypothetical protein; Complete
SEQUENCE 350 AA; 40420 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                     InterPro; IPR002723; pfam; PF01861; DUF43;
                                                                                                                                                                                                                                                                                                                                 jannaschii.";
             290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KILINWAYQQVQQNKEDAWIEHDVW 30
                                                                                                                                                                                                                                                                                             SIMILARITY: TO M.JANNASCHII MJ0675 AND T.AQUATICUS HYPOTHETICAL 38.4 kDa PROTEIN IN SCSB 5'REGION (AC P25125).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLLNNGIIRISEKKDNTWITHE-W 58
             VNWGYEEETRAWKLAPVKKKPEDIWYKSYMFRIE 323
                                  LNWAYQQ------VQQNKEDAWIEHDVWRME 33
                                                         Similarity
9; Conser
                                                                                                                                                  1PR002723; DUF43.
                                                       25.8%;
nilarity 26.5%;
Conservative
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation updat
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37.5%;
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                                                       Score 49.5; D
Pred. No. 18;
9; Mismatches
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                                                                                                   proteome.
2F301BF8976C22BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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092387; 0910A5;

30.MAY-2000 (Rel. 39, Created)

30.MAY-2000 (Rel. 39, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

VALY-LENA Myntherase (EC 6.1.1.9) (Valine-LENA ligase) (ValRS).

VALS OR CPN0094 OR CP0060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SHISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe Buropean Bioinformatics Institute. There are no restrictions on its the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shirai M., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Ishii K., Hattori M., Kuhara S., Nakazawa T.; Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CML029 from USA.",
Nucleic Acids Res. 28:12311-214 (2000).
Nucleic Acids Res. 28:2311-214 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20150255, PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Meidman J., Khouri H., Craven B., Bowman C., Grinn M., Nelson W., Deboy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.,
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                                                                                                                                                                                                                                                                                                                                                                               EMBL; AE001595; AAD18247.1; -.
EMBL; AE002226; AAF38490.1; -.
EMBL; AP0022545; BAA98304.1; -.
HSSP; P96142; IGAX.
TIGR; CP0680; -.
                                                                                                                                                                                                                    InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_l.
InterPro; IPR002303; tRNA-synt_val
Pfam; PF00133; tRNA-synt_l; 1.
PRINTS; PR00986; TRNA-SYNTHVAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
    BINDING
                                                                                        Complete
                                                                                                                                Aminoacyl-tRNA synthetase;
                                                                                                                                                           TIGRFAME; TIGR00422; vals; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 28:1397-1406(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99206606; PubMed=10192388;
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                                                                                                                       Protein biosynthesis; Ligase; ATP-binding;
"KMSKS" REGION.
ATP (BY SIMILARITY).
                                                              "HIGH" REGION
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Dodson R.
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OM protein - protein search, using sw model

49.5

F86502 B72120 T20642 E87998

hypothetical prote protein F09C3.1 (1

alyl tRNA sy valine-tRNA

tRNA syntheta ne-tRNA ligase

tRNA pseudouridine

Copyright

GenCore version 5.1.4\_p5\_4578 (c) 1993 - 2003 Compugen Ltd.

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Maximum Match 100%
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Perfect score:
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Fred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Matches

12;

Conservative

Query Match Best Local Similarity

32.6%; Score 62.5; 25.0%; Pred. No. 1. 17;

Mismatches

4. Length Indels

15;

Gaps

2

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DB

2;

480;

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10 RKTYRLKIPAKVSIDGKEYKVLDWSYEGFRIEKSKEDVFEKDKVYKVK 57

1 RRSYR-----YKLLNWAYQ--QVQQNKEDAWIEHDVWRME 33

S40764

Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:9819666; PMID:9537320
A;Accession: B70446
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-480 -A/Ey
A;Cross-references: GB:AE000751; NID:92984013; PIDN:AAC07560.1; PID:92984016; GB:AE000657
A;Exnerimental source: strain VFS

D.E., Š

A;Experimental source: strain C;Genetics: A;Gene: aq\_1687

hypothetical protein ZCS12 3 - Caenorhabditis elegans
Cipbesiss Caenorhabditis elegans
Cipbesis 6: Feb-1993 #sequence\_revision 06-Feb-1995 #text\_change 24-Nov-1999
Cibcossion: 8. Ainscough, R.
Bibmitted: 7: 18 Ainscough, R.
Bibmitted: 10: 10: ENBL Date Library, February 1993
A. Meference numbe: 540759
A. Meference numbe: 540759
A. Meference Statistical Company (1993)
A. Meference numbe: 540759
A. Meference numbe: 540759

A;Introns: 199/1; 238/1; 290/2; 529/3; 557/3; 588/3; 677/2; 733/3; C;Superfamily: Caenorhabditis elegans hypothetical protein ZK512.3

EMBL: Z22177; NID: g297989; PID: g297992

A; Molecule type: DNA A; Residues: 1-1418 < HAW>

C;Genetics: A; Cross-references:

S

15 QVQQNKED---AWIEHDVWRMEI 34

Matches Query Match Best Local &

10;

Conservative

Local Similarity

43.5%;

; Score 58.5; ; Pred. No. 19 5; Mismatche

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2; Length 1418;

772/3; 846/3; 946/1; ]

Mismatches

S

Indels

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Gaps

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hypochetical protein ad 1687 - Aquifex aeolicus
C:Species; Aquifex aeolicus
C:Date: 00-Nay-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70446
R;Deckett, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                   48.55
                                                                                                                                                               4444
                                                                                                     A82691
A82069
H84700
T40609
AE2032
H88449
T00133
C90257
                                                                            ALIGNMENTS
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                                                                                                            RNA-directed RNA p
translation initia
hypothetical prote
hypothetical prote
conserved hypothet
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RESULT B70446

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C;Species: Melanoplus sanguinipes encompoxyrius
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_chan
C;Accession: T28409
R;Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.;
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes encompoxyrius.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. BEON. S. Brouiller S. Bruschi C. V. Caldwell, B. Capusio V. Carter, M.M., Che R. Brick, S. D. Emmerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrari, E. Nature 330, 249-256, 1997 Fitz, C., Fujita, M., Enjita, Y., Fuma, S., Galizzi, A., Galler i. A., Hardhors: Foulgor, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galler i. Cett., J. Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F. Koetter, P., Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, Y. M., Ogawa, K., Ogiwara, A., Oudega, B., Fark, S.H., Farro, V., Fohl, T.M., Portetelle Rieger, M., Rivolta, C., Rocha, B., Rose, M., Sadale, Y., Sato, T., Scanlou, A., Authors: Schleich, S., Schroeter, R., Socffone, F., Schiguchi, J., Schowska, A., Serou skeuchi, M., Tamakoshi, A., Tamakashi, A., Tartie, P., Tamakoshi, A., Tamakashi, A., Ta
RESULT 5
S49113
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galactosamine-containing minor teichoic acid biosynthesis ggaB - Bacillus subtilis
G;Bpecies: Bacillus subtilis
G;Becies: D5-Dec-1997 #Hequence_revision 05-Dec-1997 #text_change 15-Oct-1999
G;Bate: D5-Dec-1997 #Hequence_revision 05-Dec-1997 #text_change 15-Oct-1999
G;Abte: D5-Dec-1997 #Hequence_revision 05-Dec-1997 #text_change 15-Oct-1999
G;Abte: D5-Dec-1997 #Hequence_revision 05-Dec-1997 #text_change 15-Oct-1999
G;Abte: D5-Dec-1997 #Hext_change 15-Oct-1999
G;Abte: D5-Dec-1997 #Hext_change 15-Oct-1999
G;Abte: D5-Dec-1997 #text_change 15-Oct-1999
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C.Species: Melanoplus sanguinipes entomopoxutrus
C.Pates: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated A;Molecule type: DNA
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Best Local Similarity
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                                                                                                                                                                                                                       59 KIKNWLYY-----NDPWIEHSKW 76
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Pred. No.
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Pred.
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A; Residues: 1-152 < KLE>
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C69546
hypothetical protein AF2371 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 22-Oct-1999
C;Accession: C65546
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Thes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z28337; NID:g509352; PIDN:CAA82191.1; C;Superfamily: Microcystis aeruginosa hypothetical protein 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-502 < JUE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: S49112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1993 A;Description: Sequence of the cyanobacterial plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S49113
R;Juerchott, K.; Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypotherical protein 2 - Microcygatis aeruginosa
C:Species: Microcygatis aeruginosa
C:Date: 01-Feb_1995 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                                                                                                                                                                                    392 QAYREKLIGWAVWRYLDGEPCQLPEEFKALQAEANKQWENNDSWEDEL 439
                                                                                                                                                                                                                                                 2 RSYRYKLLNWA------YQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                         28.9%;
25.0%;
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Pred. No. 16
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Fixlenk H.P. Clayton, R.A., Tomb, J.F.; White, O.; Nelloon, K.E.; Ketchum, K.A.; Dodson, J. Platechmann, R.D.; Quackenbush, J.; Lee, N.H.; Stutton, G.G.; Gill, S.; Kirkness, E.F.; Nature 30 (1947). L.; Dyverbeek, R.; Gooayne, J.D.; Weidman, J.F.; McDonald, L. Nature 30 (1947). Good R.; Good R.; Good R.; R.; Good R.D.; Spriggs, T.; Artiach, P.; Kaine, B.F.; Sykes, S.N. Shath, N.J. Wosee, C.R.; Venter, J.C.; Spriggs, T.; Artiach, P.; Kaine, B.F.; Sykes, S.N. Rith: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A; Reference number: A69260; Mill: 98049343; PHID: 9389475

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Cross-references: GB:AE001112; GB:AE000782; NID:g2689435; PIDN:AAB91296.1; PID:g265072: Similarity 27.6%; 42.9%; Score 53; DB Pred. No. 9.4; 6; Mismatches DB 2; Length 152;

Conservative

0

hypothetical protein ygkC - Bacillus subtilis C:Species: Bacillus subtilis C:pate: 05-Dec\_1997 #sequence\_revision 05-Dec-1997 #text\_change 15-Oct-1999

C.Accession: B69966.
R;Kunstr. P.; Ogaswara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertert R;Kunstr. P.; Capuano, V.; Carter, N.M.; Choi C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

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pioribol ester-binding protein unc-13 - Caenorhabditis elegans (**,Species: Caenorhabditis elegans (**,Species: Caenorhabditis elegans (**,Species: D-Nar-1992 #text_change 23-Feb-1997 (**,Date: 20-Nar-1992 #text_change 23-Feb-1997 (**,Accession: A41101 R**,Partynama, I.N., Brenner, S. R**,Partynama, I.N., Brenner, S. Proc. Natl. Acad. Sci. U.S.A. 88, 5729-5733, 1991 Proc. Natl. Acad. Sci. U.S.A. 88, 5729-5733, 1991 A;Ttle: A phorbol ester/diacy/glycerol-binding protein encoded by the unc-13 gene A;Reference number: A41101, MUID:91288538; PMID:2062851 A;Accession: A41101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypocherical protein ZKS24.2a - Caenorhabditis elegans C;Species: Caenorhabditis elegans c;Secies: Caenorhabditis elegans for c;Pate: 15-Oct-1999 #eequence_revision 15-Oct-1999 #rext_change C;Accession: T19295; T19931; T27889

R;Gardner, A.

Bubmitted to the EMBL Data Library, September 1996
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A,FResidues: 1-1734 <MAR>
A,FTOSE-references: GB:M62830
C.Superfamily, protein kinase C zinc-binding repeat homology
C.Supwords: phosphoprotein
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A;Experimental source: strain 168
C:Genetics:
A;Gene: yqkC
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A,FACCESSION: E59966
                                                                                                                                                                                                                                                    A; Reference number: Z19198
A; Accession: T19931
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Statue: preliminary; translated from GB/EMBL/DDBJ
A;Wolecule type: DNA
A;Wolecule type: DNA
A;Residues: 1-1813 -WIL-
A;Cross-references: EMBL;279694; PIDN:CAB01966.1; GSPDB:GN00019; CESP:ZK524.2a
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A; Accession: T19295
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A; Residues: 1-79 < KUN>
                                        A, Experimental source: clone C44E1
                                                                                 A;Residues: 1-1813 <WI2>
A;Cross-references: EMBL;Z92779; PIDN:CAB07173.1; GSPDB:GN00019; CESP:ZK524.2a
                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                     A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, March 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 NWRYDSIQEEDNEKDNWKQH 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 27.1%; Score 52; DB 2; Local Similarity 40.0%; Pred. No. 1.7e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 QNHPYTLLHWSIGGAESIKKDVWLLQDEMTFE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 NWAYQQVQQ--NKEDAWIEH 27
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9; Conserv
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R.Tomb, J.F., Milte, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A., McKenney, son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Pujli, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
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A;Cross-references: GB:BA000019; PIDN:BAB74068.1; PID:g17131461; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
                                                                                                                                                                                                                                                                                             R.Kaneko, T., Nakamura, Y., Wolk, C.P., Kuritz, T., Sasamoto, S., Watanabe, A., Iriguchi, Nakazaki, N., Shimpo, S., Sugimoto, M., Takazawa, M., Yamada, M., Yasuda, M., Tabata, S. DNA Res. 9, 205-213, 2001

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Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A, Faterence number: AB1807; MUID:11599285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypochetical procesin asr2369 [imported] - Nostoc sp. (strain PCC 7120) C.Species; Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 c;ate: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 c;ate: 14-Dec-2001 #sequence_revision 14-Dec-2001 ftext_change 30-Jun-2002 c;ates: 14-Dec-2001 #sequence_revision 14-Dec-2001 ftext_change 30-Jun-2002 c;atesision: Asi2103
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C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 16-Feb-2001
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C;Species: Helicobacter pylori
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A;Residues: 1-1813 <WI3>
A;Cross-references: EMBL:Z73912; PIDN:CAA98147.1; GSPDB:GN00019; CESP:ZK524.2a
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A, Accession: T27889
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C;Superfamily: Pseudomonas D-amino acid hydantoin hydrolase (ATP-hydrolyzing) hyuA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                          A; Molecule type: DNA
A; Residues: 1-90 < KUR>
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Best Local 9
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Pred. No. 76;
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C;Species: Caen
C;Date: 15-Oct-
C;Accession: T2
R;MCMurray, A.
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A;Introns: 332/1; 416/3
C;Superfamily: human GDP dissociation inhibitor XAP-4
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A,Molecule type: DNA
A,Residues: 1-1444 <WIL>
A,Cross-references: EMBL: 259281; PIDN:CAB16511.1; GSPDB:GN00022; CESP:Y57G11C.10
A,Experimental source: clone Y57G11C
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAA18354.1; PID:g165344
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: xylulokinaee
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-495 <KAN>
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A; Status: preliminary
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o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-116, 1996
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A; Accession: T27222
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C.Species: Cenorhabditis elegans
C.Pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, September 1997
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Matches 11
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                                                                                                              YEGNIVGQAYKELTQFYPKAGWVEHDALEIWR
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Pred. No. 9.
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Pred. No. 60;
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hypothetical protein PA3079 [imported] - Pseudomonas aeruginosa (strain PA01) c/species: Pseudomonas aeruginosa (c/species: Pseudomonas aeruginosa (species: Pseudomonas aeruginosa PA01, an opportunistic pathog A;Pateries romaber: A82950; MUID:20437337; PMID:10984043 A;Pateries romaber: A82950; MU
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BA;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal A; Meteraence mumber: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                       A;Gene: alr5031
C;Superfamily: Synechocystis hypothetical protein slr2003
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A;BXPErimental Bource: Btrain PCC 7120
C;Genetics:
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C/Species: Nostoc sp.
AlNote: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC .
AlNote: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC .
Claste: 14-bec-2001 #sequence_revision 14-bec-2001 #text_change 30-Jun-2002
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A;Experimental source: strain PAOI
C;Genetics:
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A; Residues: 1-201 < KUR>
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A;Residues: 1-793 <STO>
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LNWQISQFQQQVGE-WLEYQSYRFE
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Gapop 10.0 , Gapext 0.5
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192
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Cgn2 6/ptodate/1/pibpaa/US08 NRW PUB pep:

('Ggn2-6/ptodate/1/pibpaa/US08 NRW PUB pep:

('Ggn3-6/ptodate/1/pibpaa/US06 NRW PUB pep:

('Ggn3-6/ptodate/1/pibpaa/US06_PUBCOMB pep:

('Ggn3-6/ptodate/1/pibpaa/US07_PUBCOMB pep:

('Ggn3-6/ptodate/1/pibpaa/US07_PUBCOMB pep:

('Ggn3-6/ptodate/1/pibpaa/US07_PUBCOMB pep:

('Ggn3-6/ptodate/1/pibpaa/US08_PUBCOMB pep:

('Ggn3-6/ptodate/1/pibpaa/US09_PUBCOMB pep:

('Ggn3-6/ptodate/1/pibpaa/US00_PUBCOMB pep:

('Ggn3-6/ptodate/1/pubpaa/US00_PUBCOMB pep:

('Ggn3-6/ptodate/1/pubp
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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TO	107	107	107	107	107	192	192	192	192	192	192	192	192	192	192	192	192	192	Score
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sequence I, Appli	Sequence 13, Appl	Sequence 15, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 879, App	Sequence 879, App		Sequence 2, Appli	Sequence 2, Appli	Seguence 879, App	Sequence 879, App	Sequence 11, Appl	Sequence 879, App	Sequence 51, Appl	Sequence 50, Appl	Sequence 20, Appl	•	Description

RESULT 2 US-10-010-667A-20

i	S	44	3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	8	
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:	24.2	24.2	24.2	24.2	24.2	24.5	24.5	24.5	24.5	24.5	24.5	24.7	25.0	25.0	25.3	25.3	25.3	26.0	26.0	26.0	26.6	26.8	27.1	27.1	44.3	44.3	
į	215	215	215	215	135	1503	823	669	525	441	274	4150	825	496	654	151	151	1193	469	370	487	491	1114	38	15	15	
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			Sequence 150, App	Sequence 150, App	Sequence 1191, Ap	Sequence 1, Appli	Sequence 923, App	Sequence 1336, Ap	Sequence 79, Appl	Sequence 16, Appl	Sequence 171, App	Sequence 2, Appli	Sequence 922, App	Sequence 5483, Ap	Sequence 10, Appl	Sequence 974, App	Sequence 145, App	Sequence 2, Appli	Sequence 1494, Ap	Sequence 436, App	Sequence 3647, Ap	Sequence 128, App	Sequence 10, Appl	Sequence 38670, A	Sequence 32, Appl	Sequence 32, Appl	

## ALIGNMENTS

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US-10-011-095-20
; Sequence 20, Application US/10011095
; Publication No. US20030045682A1
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                 S
                                                                       ; OTHER INFORMATION: STEAP-1 peptide US-10-011-095-20
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                   Matches
                                            Query Match
Best Local Similarity
                                                                                         FEATURE:
                                                                                                ORGANISM: Artificial Sequence
1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                   ch 100.0%; Score 192; DB 9;
1 Similarity 100.0%; Pred. No. 1.1e-19;
34; Conservative 0; Mismatches 0;
                                                     Length 34;
                                     Indels
                                     0
                                     Gaps
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APPLICANT: Zhang Jie ...

APPLICANT: Ren Beriyen

APPLICANT: Agundi, Vinod

APPLICANT: Agundi, Vinod

APPLICANT: Damand: Red)e T

TITLE OF INVENTION: ANETHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE

TITLE OF INVENTION: LIKE POLYPEPTIDES AND POLYNUCLEOTIDES

PILE REFERENCE: HYE-JTCIP

CURRENT PILLAG DATE: 2000-03-03-08

PRIOR PELICATION NUMBER: US 09/729, 739

PRIOR PILLAG DATE: 2000-01-04

PRIOR PILLAG DATE: 2000-03-13

PRIOR PILLAG DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 09/589,042

PRIOR PILLAG DATE: 2000-03-20

PRIOR PILLAG
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CURRENT INFLINA DATE: 200112-06
PRIOR APPLIAND NUMBER: 09/22,873
PRIOR FILING DATE: 199-06-01
PRIOR APPLICATION NUMBER: 60/097,520
PRIOR PLING DATE: 1998-06-01
PRIOR PLING DATE: 1998-06-01
PRIOR PLING DATE: 1998-06-30
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Best Local Similarity
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SEQ ID NO 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50, Application US/09747835A Patent No. US20020146692A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Raitano, Arthur B.
APPLICANT: Mitchell, Steve Chappell
APPLICANT: Mitchell, Steve Chappell
TITLE OF INVENTION: MOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 511582001601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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Leong, Kahan
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Liu, Chenghua
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Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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100.0%; Pred. No. 1.1e-19;
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US-09-747-835A-50
                                                                                                                                                                                                                                                                                                                                                 US-10-012-896-879
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PRIOR FILLING DATE: 2000-12-04
PRIOR PILLING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILLING DATE: 2000-07-19
PRIOR PILLING DATE: 2000-07-19
PRIOR PILLING DATE: 2000-08-20
PRIOR APPLICATION NUMBER: US 09/558,042
PRIOR PILLING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR PILLING DATE: 2000-04-25
                                                                sequence 879, Application US/10012896
Publication No. US20020183251A1
GENERAL TIMPORANTION:
APPLICANT: US. Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hatlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 51
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
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Best Local (
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APPLICANT: Ren, Feiyan
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: DE INVENTON: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO G PROTEIN-COUPLED RECEPTOR-LIKE
FILE REFERENCE: HYS-37CIP
CURRENT APPLICATION NUMBER: US/09/747,835A
CURRENT APPLICATION NUMBER: US/09/747,835A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TYPE: PRT
     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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    Application US/09747835A
    US20020146692A1

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Liu, Chenghua
     Kalos, Michael D
                                     Jiang, Yuqiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 192;
100.0%; Pred. No. 1
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Pred. No. 1e-18;
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Marc W.

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US-09-802-520-11
Sequence 11, Application US/09802520
Publication No. US20020187472A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-012-896-879
                                                                                                                                                US-09-802-520-11
                                                                                                                                                                                                                                                        SOFTWARE: PEI
SEQ ID NO 11
LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 879
LENGTH: 339
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                                                                                                          Query Match
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lal, Preeti
APPLICANT: Faris, Mary
APPLICANT: Chen, Huei-Mei
APPLICANT: Ison, Craig H.
APPLICANT: Ison, Craig H.
TITLE DG INVENTION: STEAR-RELATED PROTEIN
FILE REFERENCE: PC-0037 US
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                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
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                                                                                        Local Similarity
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                                      1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
Henderson, Robert A.
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Li, Samuel X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roy, Teresa
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yoshihiro
                                                                                           100.0%; Score 192; DB 9; 100.0%; Pred. No. 1.3e-18;
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                                                                            Mismatches
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                                                                                                          Length 339;
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; ORGANISM: Homo sapiens 
US-09-895-793-879
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US-09-895-793-879
                                                                                                                                                                                                                                                                                                                                                                                   US-09-895-814-879
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SEQ ID NO 879
LENGTH: 339
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               Sequence 879, Application US/09895814
Publication No. US20020193296A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PRIGET, GATY R.
TITLE OF INVENTION: OMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 20121-254C2
CURRENT PILLOLION NUMBER: US/09/895,793
CURRENT PILLOLION NUMBER: US/09/895,793
RUMBER OF SEO ID NOS: 982
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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APPLICANT: Dillon, Davin C.
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  APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                  Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Carter, Darrick
Li, Samuel X.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Kalos, Michael D.
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                                                                                                                                   Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Hepler, William T.
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Vedvick, Thomas S.
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Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harlocker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09895793
b. US20020192763A1
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
                                                                                                                                                                                        Retter, Marc W. Stolk, John A.
                                                                                                                                                                                                                          Kalos, Michael D.
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                                                                                                                     Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enderson, Robert A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 339;
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PILE REPERBICE: $11582001610
CURRENT PILING DATE: 2001-12-06
REIGR APPLICATION NUMBER: 09/23/873
REIGR APPLICATION NUMBER: 09/23/873
REIGR APPLICATION NUMBER: 09/087,520
PRIOR APPLICATION NUMBER: 69/091,183
PRIOR APPLICATION NUMBER: 69/091,183
PRIOR PILING DATE: 1999-66-01
NUMBER OF SEG ID NOS: 32-99-06-01
SEG ID NO 2
SEG ID NO 2
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 31012, 447C26
CURRENT APPLICATION NUMBER: US/99/895,814
CURRENT PILLOR DATE: 2001-06-29
SUPPMARE: FREUSEO FOR WINDOWS Version 3.0
SOFTMARE: FREUSEO FOR WINDOWS Version 3.0
SOFTMARE: FREUSEO FOR WINDOWS VERSION 3.0
SEQ ID NO 8:9
                                                                 Sequence 2, Application US/10010667A Publication No. US20030055217A1 GENERAL INFORMATION:
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Publication No. US20030045682A1
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APPLICANT: Saffran, Douglas C.
APPLICANT: MITChell, Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Afar, Daniel
APPLICANT: Hubert, Rene S.
APPLICANT: Leong, Kahan
APPLICANT: Raitano, Arthur
APPLICANT: Afar, Daniel APPLICANT: Hubert, Rene S. APPLICANT: Leong, Kahan
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                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Foy, Тегева
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Pred. No. 1.3e-18;
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APPLICANT: SEFERAL DOUGLAS C.

APPLICANT: WICCHELL SERVE CHAPPEL

TITLE OF INVENTION. NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION. EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: $11692001601

CURRENT PELLORION WHOMER: US/10/010,667A

CURRENT PELLORION WHOMER: US/10/010,667A

CURRENT PELLORION WHOMER: US/10/010,667A

PRIOR APPLICATION WHOMER: US/10/01,520

PRIOR APPLICATION WHOMER: US/10/01,520

PRIOR APPLICATION WHOMER: US/10/01,520

PRIOR APPLICATION WHOMER: US/10/01,183

PRIOR APPLICATION WHOMER: US/10/01,183

PRIOR APPLICATION UNBER: US/10/01,183

PRIOR APPLICATION UNBER: US/10/01,183

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                                                                                                                              US-09-759-143-879
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                                                      Matches
                                                                  Query Match
Best Local Similarity
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LENGTH: 339
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Best Local Similarity
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CURRENT FILING DATE: 2001-01-12
CURRENT FILING DATE: 2001-01-13
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FASTSEQ for Windows Version 3.
                                                                                                                                                                                                                                                                                             APPLICANT: Skeiky, Yasir A.M.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.437C23
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                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                  TYPE: PRT
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1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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Dillon, Davin C.
Mitcham, Jennifer L.
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Carter, Darrick
Li, Samuel
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Kalos, Michael D.
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Pred. No. 1
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Pred. No. 1.3e-18;
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RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-780-669-879
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US-09-822-827-879
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US-09-822-827-879
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                                                                                                                        CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 899
LENGTH: 339
                                                                                                                                                                                                                                     Sequence 879, Application US/09822827

PATENT NO. US20020081680A1

REFIGURATE: AU. Jiangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFERENCE. 21012.1.54c1
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LENGTH: 339
  Matches
                                     Query Match
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CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIACNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
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                    Local Similarity
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les 34; Conserv
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34; Conservative
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Hepler, William
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Kalos, Michael D.
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McNeill, Patricia D.
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Conservative 0
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                    100.0%; Score 192; DB 10; 100.0%; Pred. No. 1.3e-18;
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Pred. No. 1.3e-18;
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US-09-963-896-1
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                                                                                                                                                                                                            RESULT 15
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GENERAL INFORMATION:
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                Sequence 8, Application US/10011095
Publication No. US20030045682A1
                  APPLICANT:
APPLICANT: Raitano, Arthur B.
APPLICANT: Saifran, Douglas C.
APPLICANT: Mitchell Steve Chappell
TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAPI (AS AMENDED)
                                                                             APPLICANT:
                                                                                             APPLICANT:
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TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/397,558
PILLING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/963,896 FILING DATE: 26-Sep-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 39,132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: CERRONE, MICHAEL C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: PROSTUT10
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                                                                     Hubert, Rene
Leong, Kahan
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                                                                                             Rene S.
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Pred. No. 1.8e-07;
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CURRENT PILLING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 09/323,873
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Maximum Match 100%
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1. /cgn2 c/prodata/1/iss/5A COMB.pep:*

2. /cgn2 c/prodata/1/iss/5B COMB.pep:*

3. /cgn2 c/prodata/1/iss/6B COMB.pep:*

4. /cgn2 c/prodata/1/iss/6B COMB.pep:*

5. /cgn2 c/prodata/1/iss/PCTUS COMB.pep:*

5. /cgn2 c/prodata/1/iss/PCTUS COMB.pep:*
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1 RRSYRYKLLNWAYQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
        GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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  Sequence 2, Application US/09323873A
Patent No. 632503
GENERAL IMPROMATION:
APPLICANT: Deniel B. Afer
APPLICANT: Bene S. Hibbert
APPLICANT: Rene S. Hibbert
APPLICANT: Athur B. Raitano
APPLICANT: Athur B. Raitano
APPLICANT: Seve Chappell witchell
APPLICANT: Seve Chappell witchell
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§ 0,	Gaps	0;	Length 34; Indels	100.0%; Score 192; DB 4; ilarity 100.0%; Pred. No. 3.7e-20; Conservative 0; Mismatches 0;	uery Match est Local Similarity atches 34; Conser
				E: INFORMATION: STEAP-1 PEPTIDE 873A-20	FEATURE: OTHER INFORMATI 09-323-873A-20
				Principal Company	LENGTH: 34 TYPE: PRT
				NOS: 32 Q for Windows Version 4.0	NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ for
				APPLICATION NUMBER: 60/091,183 FILING DATE: 1998-06-30	
				2 🚡	PRIOR APPLICATION OF THE PRIOR PRIOR PRIOR PRIOR DATE
				FILING DATE: 1999-06-01	CURRENT APPLICATION
		OF.	ANTIGENS USES THEREOF	NOVEL SERPENTINE TRANSMEMBRANE EXPRESSED IN HUMAN CANCERS AND LENGTH	
				fran   Mitchell	
				. 0 7	
				3 ON: LE. Afar	atent No. 6329503 ENERAL INFORMATION: APPLICANT: Daniel E.
				ication US/09323873A	ULT 1 09-323-873A-20 equence 20, Applicat
				ALIGNMENTS	
Appli	4.	nce	Sequence	7 2304 4 US-09-324-	43.5
9, Ap	16,	nce	Seguence	7 7	44 43.5 22
Appli	N	nce	Seguence	7 438 4 US-09-072-917A-	43.5
Appli	•	nce	Sequence	7 438 1 US-08-343-380-2	43.5
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	445	nce	Sequence	9 476 4	4.
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Appli	1,0	nce	Sequence	9 372 2 US-08-884-	44
App	114	) ince	Sequence	9 368 4 US-09-056-556-	4 4
	109,	nce	Sequence	9 368 4 US-08-818-111-	29 44 22.
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PILE REPRENCE: 129.45USUZ
CURRENT APPLICATION NUMBER: US/09/323,873A
CURRENT PILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: 60/087.520
PRIOR PILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-06-01
PRIOR PILING DATE: 1999-06-03
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US-09-323-873A-2
                                                                                                                                US-09-083-521-1
                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:

NAME CERRONE, MICHAEL C.

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0527 US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEPHONE: (650) 854-4166

INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09083521
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    Matches
                                  Best Local
                                                                Query Match
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TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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HEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATINA SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MOA'D PEFECU 6.1 for Windows/MS-DOS 6.2

CHRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
APPLICANT: COR'Ley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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Local Similarity 100.0%; Pred. No. 4.9e-19;
nes 34; Conservative 0; Mismatches 0;
                                                                                                                                                     CLONE: 1691243
                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: Herewi
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nilarity 58.8%;
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Score 107; DB 3; Length 141; Pred. No. 1e-07; 5; Mismatches 9; Indels
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                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-323-873A-32
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LENGTH: 173
                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 15
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    Query Match
Best Local Similarity
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APPLICANT: Douglas C. Seffran
APPLICANT: Bouglas C. Seffran
APPLICANT: Seve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.16USU2
CURRENT APPLICATION UNMER: US/09/323,873A
CURRENT PILING DATE: 1998-06-01
RIOR APPLICATION UNMER: 05/087,520
PRIOR APPLICATION UNMER: 09/08-01
                                                                                                                                                                                                                                                                                                                                                                       NPELICANT: Arthur B. Reiteno
APPLICANT: Douglas C. Saffran
APPLICANT: Steve Chappell Mitchell
APPLICANT: Steve Chappell Mitchell
TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
TITLE OF INVENTION: EXPERSION IN HUMAN CANCERS AND USES THEREOF
FILLE REFERENCE: 129.16USU2
CURRENT APPLICATION WHERE: US/09/323.873A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION WHERE: 60/087.520
PRIOR APPLICATION WHERE: 1999-08-01
PRIOR APPLICATION WHERE: 1999-08-01
PRIOR APPLICATION WHERE: 1999-08-01
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/091,183
PRIOR FILING DATE: 1998-06-30
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APPLICANT: Rene S. Hubert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Daniel E. Afar
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ORGANISM: Homo Sapiens
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Kahan Leong
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Pred. No. 1.3e-07;
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        Score 85;
Pred. No.
            DB 4; L
9.1e-06;
                                      Length 15;
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EMALIER APLICATION UNDER: 00/040,33  EMALIER APLICATION UNDER: 00/040,626  EMALIER APLICATION UNDER: 00/040,626  EMALIER APLICATION UNDERE: 60/040,626  EMALIER APLICATION UNDERE: 60/040,334  EMALIER APLICATION UNDERE: 60/040,334  EMALIER APLICATION UNDERE: 60/040,336  EMALIER APLICATION UNDERE: 60/040,336  EMALIER APLICATION UNDERE: 60/040,600  EMALIER APLICATION UNDERE: 60/040,600  EMALIER APLICATION UNDERE: 60/040,600  EMALIER APLICATION UNDERE: 60/040,600  EMALIER APLICATION UNDERE: 60/047,600  EMALIER APLICATION UNDERE: 60/047,600  EMALIER APLICATION UNDERE: 60/047,502  EMALIER APLICATION UNDERE: 60/047,603  EMALIER APLICATION UND	15; CONSERVE VOOVOONKEDAWIE VOOVOONKEDAWIE VOOVOONKEDAWIE VOOVOONKEDAWIE VOOVOONKEDAWIE VOOVOONKEDAWIE VOOVOONKEDAWIE VOOVOONKEDAWIE VALUE VOOVOONKEDAWIE VO
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                RQRKLNDALDRLEELKEFANFDFDVWR 217
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                                                                                                                                                                                                                           APPLICATION NUMBER: 60/049,610
                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/057,669
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/056,884 FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                        APPLICATION NUMBER: 60/061,060
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                                                                                                          26.0%; Score 50; DB 4; Length 370; 40.7%; Pred. No. 23;
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LOCATION: 1..654
OTHER INFORMATION:
US-08-560-005-10
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                                                                                                                                                                                                                                                                     US-09-418-540-10
                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                             Sequence 10,
Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307
TELECOMMUNICATION: TOPORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPTER READABLE FORM;
MEDIUM TYPE: Floppy disk
COMPTER: IBM PC compatible
ORENTING SYSTEM: PC COMPA: DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
APPLICATION DATA:
APPLICATION UMBER: US/00/560,005
                                                                                          APPLICANT: Pot. David A.
APPLICANT: Williams, Lewis T.
APPLICANT: Affectson, Anne Bennett
APPLICANT: Majerus, Philip M.
APPLICANT: Majerus, Philip M.
APPLICANT: Majerus, Philip M.
TITLE OF INVENTION: Acids Encoding Therefor
TITLE OF INVENTION: Acids Encoding Therefor
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APPLICANT: Majerus, Philip W.
TITLE OF INVENTION: No. 600154el Grb2 Assoc
TITLE OF INVENTION: Acids Encoding Therefor
                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                          NUMBER OF SEQUENCES:
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STREET:
CITY: S
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STATE: California
                ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                                   3 SYRYKLLNWAYQQ----VQQNKEDAWIEHDVWR 31
San Francisco
                                                                                                                                                                                                                                                Application US/09418540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08560005
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Williams, Lewis T.
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25.0%; Pred. No. 70;
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Length 654; Indels

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STATE:

California

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; LOCATION: 1..654
; OTHER INFORMATION:
US-09-418-540-10
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Best Local Similarity
Thes 8; Conserv
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                                                                                                                                                                              ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3412, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3412
LENGTH: 178
                                                                                                         Matches
                                                                                                                                         Query Match
                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 199-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION MYMBER: US 08/560,005
FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: DOW, KAFER B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-0624
TELECOMMUNICATION INFORMATION:
TELEPHÓNE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: LYAN DOUGETE-SEAMM Et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: GTC-007
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acid
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 TYKYRGRDYAYKQKDTSEKTRVPAWCDRILWK 379
                                    139 RONHSKSQSDWNHQQNQQHK-DAW 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 14-OCT CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 SYRYKLINWAYQQ----VQQNKEDAWIEHDVWR 31
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                                                                       1 RRSYRYKLLNWAYQQVQQNKEDAW 24
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amino acid
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                                                                                                                          24.7%;
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Pred. No. 70;
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Pred. No. 2:
                                                                                                         Mismatches
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; Sequence 4, Application US/09332319
. Ratent No. 6171821
; GENERAL INFORMATION:
. APPLICANT: KOTNELUK, Robert G.
. APPLICANT: HOLCIK, Martin
                                                                                        RESULT 12
US-09-332-319-4
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US-09-428-517-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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Query Match
Best Local Similarity
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APPLICANT: McDaitel. Robert
ITITLE OF INVESTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-2002-00
CURERRY APPLICATION NUMBER: US/09/428,517
CURRERY FLING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER PILING DATE: 1999-02-16
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER PILING DATE: 1999-02-16
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EARLIER PILING D
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APPLICANT: HOLCIK, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THERBOF
FILL REFERENCE: 07891/021001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/121,979
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 4
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APPLICANT: Shah, Sanjay Krishnakant
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1924 RYWLLDKAAORERERLED-WRYHVEWR 1949
46 LANW-----KPKEDPWEQHAKW 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 RYKLLNWAYQQVQQNKEDAWIEHDVWR 31
                                                                              8 LINWAYQQVQQNKEDAWIEHDVW 30
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5. 6251636
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Pred. No. 7.7e+02;
4; Mismatches 10
                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                   Score 46;
Pred. No.
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APPLICANT. Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TITLE OF INVENTION: MALE PERTILITY
FILE REFERENCE: 07891/018002 F1127
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/673,001
PRIOR FILING DATE: 1998-01-29
INUMBER: 0780 IN 1008: 10
SOFTWARE: FRESER FOR WINDOWS Version 4.0
SEQ ID NO 3
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US-09-239-867-2
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US-09-239-867-2
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LENGTH: 236
TYPE: PRT
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GENERRAL INFORMATION:
APPLICANT: Robert G. Korneluk et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08746789A Patent No. 5789200
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CHERENT APPLICATION WINDER: US/09/322,319
CHERENT FILING DATE: 1999-06-14
EARLIER APPLICATION WINDER: 09121,979
EARLIER FILING DATE: 1998-07-24
WINDER OF SEQ ID NOS: 30
ONTWARE: JeseSEQ for Windows Version 3.0
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TITLE OF INVENTION: XIAP IRES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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APELICANT: ISMAIL KOLA, Martin J. Tymma, APELICANT: ISMAIL KOLA, Martin J. TYMMAR TITLE OF INVENTION: A 40. 5789200el Human ETT NUMBER OF EQUINORES 4

CORRESPONDENCE ADDRESS: SMITHKING Beecham Corporation ADDRESSEE: SMITHKING Beecham Corporation ADDRESSEE: SMITHKING BEECHAM CORESPONDENCE ADDRESSEE: SMITHKING BEECHAM CORPORATION ADDRESSEE: SMITH
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                                  ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM 486
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nes 9; Conservative
    OPERATING SYSTEM:
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WINDOWS FOR WORKGROUPS
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Pred. No. 50;
2; Mismatches
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APPLICANT: Cohoon, Rebecca E.
APPLICANT: Odell, Joan
APPLICANT: Refaleki, Antoni
TITLE OP INVENTION: Transcription Coactivators
FILE REFERENCE: BB-116-18
CURRENT PELLOTION UNMERS: U9/09/342,648
CURRENT FILING DATE: 1099-06-29
EARLIER APPLICATION UNMERS: 06/092,659
EARLIER FILING DATE: 1017 13, 1998
UNMERS OF ERGO LD NOS: 10
SOFTARE: Microsoft Office 97
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Best Local S
Matches 8
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LENGTH: 885
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610 270 4026 INFORMATION FOR SEQ ID NO:
                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/746,789A
FILING DATE: No. 5789200ember 15
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REFERENCE/DOCKST NUMBER: ATTELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5219
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
611
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mes 8; Conserv
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                            2 RSYRYKLLNWAYQQVQQNKEDAWIEHD 28
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RSSYYKSLLSAEEAAKOKKEKVWAHYE 637
                                                             10;
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                                                                Conservative
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Pred. No.
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Pred. No. 3e+02;
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Search completed: March 26, 2003, 16:51:40 Job time: 22.7442 secs

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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1: Sp_archea:*
2: Sp_bacceria:*
3: Sp_fungi:*
4: Sp_hunan:*
5: Sp_invertebrat
6: Sp_manal:*
7: Sp_mbc:*
8: Sp_organelle:*
8: Sp_bhage:*
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Gapop 10.0 , Gapext 0.5
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196.889 Million cell updates/sec
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12:
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192
1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
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sp_unclassified:*
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sp_archeap:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11 11 11 11 11 11 11 11 11 11 11	Result No.
192 187 187 189 109 109 109 60.5 96.5 96.5 96.5 58.5 57.5	Score
100.0 100.0 97.4 97.4 72.4 72.4 56.8 56.8 56.3 31.2 31.2 31.2 31.2 29.9	Query Match
264 338 339 339 339 488 488 488 488 488 926 1027 1027	% Query Match Length DB
12 4 4 4 11 11 11 12 12 12 12 12 12 12 12 12 12	BB
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Q9hzc9 pseudomonas				26	51	38
QBusu8 human immun			۰.		51	37
Q21449 caenorhabdi	o		•	26	51	36
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Q8rpu7 klebsiella				26	51	4
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Q8yuh7 anabaena sp	16 Q8YUH7		.6	26	51	3
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025402 helicobacte				26	51.5	30
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Q9g045 mycobacteri	Ω		_	26	51.5	28
Q9wf65 human immun		1427 1	.1		52	27
Q9w296 drosophila	_		.1 12		52	8
Q9fhe5 arabidopsis			.1		52	5
Q9n7a8 leishmania	n		; ,		52	24
Q9iwq0 human immun				27	52	23
Q8ttf0 methanosarc			.6	27	53	22
O87519 escherichia	0		-	27	53	2
O30299 archaeoglob	17 030299		•	27	53	8
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Q48904 microcystis	_	502 2	_	28	55.5	18
Q9rfp3 mycoplasma	2 Q9RFP3	230 2	N	29	56	17

## ALIGNMENTS

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y Match Local hes 3	NON TER SEQUENCE	00	73	Strong C., Layman D., "The sequence of Homo Submitted (JUN-1998) (	[2] SEQUENCE FROM N.A.	Sulston J.E., Water	SEQUENCE FROM N.A. MEDLINE=99063792;	NCBI_TaxID=9606;	Eukaryota; Metazoa; Mammalia: Eutheria:	WUGSC:H_RG087E15.1.	01-DEC-2001	01-NOV-1999	Q9Y6US	H L
100.0%; Similarity 100.0%; 4; Conservative	264 264 264 AA; 31203 MW;	(DEC-1999) to the 5061; AAD43182.1;	N.A.	បីខ្លួក	[2] SEQUENCE FROM N.A.	Sulston J.E., Waterston R.; "Toward a complete human genome	OM N.A. 63792; PubMed=9847074;		Metazoa; Chordata; utheria; Primates;	WUGSC:H_RG08/EIS.I procein WUGSC:H_RG087E15.1. Homo ganiene (Human)	(TrEMBLiel 19,		PRELIMINARY;	
Score 192; Pred. No. 0; Mismatch	MW; 35C9483003557E72	ne EMBL/GenBank/DDBJ l;		Graves T., Strowmatt C.; sapiens BAC clone CTB-87E15. o the EMBL/GenBank/DDBJ data	,	jenome sequence.";	847074;			(Fragment).	, Last	Creat	PRT; 264	
DB 4; Length Be-17; 0; Indels	3557E72 CRC64;	/DDBJ databases.		tt C.; CTB-87E15."; /DDBJ databases.		. 11 /			Craniata; Vertebrata; Eutele Catarrhini; Hominidae: Homo.		annotation update)		AA.	
264; 0; Gaps								٠	Euteleostomi;					

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A Makawa T., Hara M., Pukunishi Y., Komno H., Adachi J., Pukuni S.,
A Mizawa K., Izawa W., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
A Mizawa K., Izawa W., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
A Mizawa K., Izawa W., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,
A Mizawa K., Kateuda H.A., Ashburner M., Bacalov S., Casavent T.,
A Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
A Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,
A Kuehi P., Lewis S., Matsu V., Nikaido I., Peole G., Quackenbush J.,
A Kuehi P., Lewis S., Matsu V., Nikaido I., Peole G., Quackenbush J.,
A Kuehi P., Lewis S., Matsu V., Nikaido I., Peole G., Quackenbush J.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarali R., Bareh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
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A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Suzuki H., Toyo-oka K., Wang K.H., Meirz C., Mintsker C.,
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Matches 34
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Q9CWR7;
Q1-SUN-2001 (TrembLrel 17,
01-JUN-2001 (TrembLrel 17,
01-DEC-2001 (TrembLrel 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-C57BL/6J; TISSUE-EMBRYONIC STEM CELLS;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Six transmembrane endothelial antigen of PAEC.
   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21085660; PubMed=11217851;
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                                 Nachre
                                                    Hayashizaki Y.; "Function of a full-length mouse
                                                                                                        Wynshaw-Boris A., Yoshida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
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       AK010437;
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                                 409:685-690(2001
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J.-P., Charreau
                                                                                                            K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Last sequence update)
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Pred. No. 3.7e-17;
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Sciurognathi; Muridae;
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                                                        cDNA collection.";
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; Murinae; Mus
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Matches 32
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Matches 32; Conserv
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01-DEC-2001
01-JUN-2002
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Cancer Res. 6:1587-586 (2001).

EMBL, A2297098, AXE3116-1;
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SEQUENCE 339 AA; 39264 MW;
                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                    Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL, AV029584, AAK50537 1; -
                                                                                                                                  "Prostate and non-prostate of human STEAP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q924Z2;
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Six-transmembrane epithelial
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                                                                                                                                                                                                                     Manivet P.,
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                         (Mouse)
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Rodentia;
                                                                                                                                                                                                                                                                                                                                 Chordata;
Rodentia;
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                                 39109 MW;
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                                                                                                                                                                                                                        Lamblin
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                                                                                                                                                                expression
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Last annotation updat
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Pred. No. 1
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Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi; Muridae; Murinae; Mus
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                                 32A2C29F2E333BD0 CRC64;
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1.6e-16;
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1.6e-16;
hes 0;
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Best Local :
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099941; O1-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2002 (TremBlrel. 21,
                                                                                                                                                                                                                                                                                                               Q924Z1
Q924Z1,
                                                                                                                                                                                                                                                                           01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A novel prostate cancer associated gene.";
Submitted (FBR-2000) to the EMEL/GenBank/DDBJ databases.
EMBL, AR335281, AAK80351.1;
EMBL, AR335281, AAK80351.1;
SEQUENCE 488 AA, 54640 MM; 59FF07121919FDCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=DUNNING; TISSUE=PROSTATE CANCER TUMOR;
Lu Y., Rinaldy A.R., Steiner M.S.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Growth inhibition of prostate cancer by an adenovirus expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=DUNNING; TISSUE=PROSTATE CANCER MEDLINE=20424188; PubMed=10969787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor suppressor pHyde.
Rattus norvegicus (Rat).
            SECUENCE FROM N.A.
SECUENCE FROM N.A.
SETTU V., Lamblin D., Lenoir C., Manivet P., Vaubourdoll
Kellermann O., Loric S.;
Wolecular cloning and expression of mouse dudulin 2.";
Wolecular cloning and expression of mouse dudulin 2.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AY029586; AAK59539.1;
EMBL; AY029586; AAK59539.1;
                                                                                                                                                               Eukaryota, Metazoa,
Mammalia, Eutheria,
                                                                                                                                                                                                                                         Dudulin 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       novel tumor suppressor gene, pHyde.", Cancer Res. 60:4419-4425(2000).
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                                                                                                                                        NCBI_TaxID=10090
                                                                                                                                                                                                   Mus musculus (Mouse)
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MGI:1915678; 1010001D01Rik.
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nilarity 73.5%;
Conservative
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A.R., Steiner M.S.;
                                                                                                                                                               Chordata;
Rodentia;
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Pred. No. :
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Pred. No.
                                                                                                                                                               Craniata, Vertebrata, Euteleostomi, Sciurognathi, Muridae, Murinae, Mus
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                                                                                         Vaubourdolle
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01-JUN-2002
01-JUN-2002
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EMBLI, AVO29158; AAK50539.11 -
INGERTE, PROCUSOS, IG AMGC, INNKNOWN 1.
EROUSOS, IG AMGC, INNKNOWN 1.
EROUSOS, IG AMGC, INNKNOWN 1.
EROUSOS, IG AMGC, INNKNOWN 1.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSWNES.
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DCT-2000 (TrEMBLrel. 19, Last sequence update)
CDNA FLJ10829 fls, clone NTZRF4001138 (Dudulin 2).
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                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagi K., Sugano S., Aotsuka S., Yoshikawa Y., Mishikawa Y., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamats Makamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEDO human Chuk sequencing project ",
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                   SEQUENCE
                                                                  Wang C., Allay J.A., Steiner M.S.;
"Second human member of pHyde family, Human pl
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                   Bukaryota; Metazoa;
Mammalia; Butheria;
                                                                                                                                                                                                                                         PHYDE II
                                                                                                                                                                                                                                                                                                                 QBTDP3;
                                                                                                                                                                                                                                                                                                                                   Q8TDP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Dudulin 2, a new tumor antigen expressed in various hum
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9NVB5
                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                       Homo sapiens (Human)
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Vaubourdolle M., Kellermann O., 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RRSYRYKLINWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                           RRAHRYDLVNLAVKQVLANKSHLWVEEEVWRMBI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRSHRYDLVNLAVKQVLANKSRLWVEEEVWRMEI 359
                                   AF262322; AAM08128.1; -
NCE 456 AA; 50430 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 AA;
                                                                                                                                                                                                                                                         (TrEMBLrel.
(TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57268 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.7%;
50.3%;
                                                                                                                                                                                                                                                           21,
                                                                                                                                                                                                                                                         Created)
Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 4; L
Pred. No. 6.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 109; DB 11;
Pred. No. 3.8e-06;
  Score 96.5;
                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339886C288AEC0E2
                                   C5F7C7008D55251E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Eschwege
Loric S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 488;
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Length 456;
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    RESULT: 12
                                                                                                                                                                                                        Query Match
Best Local S
Matches 12
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Matches 19
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Matches 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OBTF03; PRELIMINARY;
OBTF03;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ_1687.
Aquifex aeolicus.
Bacteria; Aquificae; A
NCBI_TaxID=63363;
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067595;
01-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Steiner M.S., Allay J.A., Mang C.;
"A novel prostate-derived tumor suppressor.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, NR23864; AAL/8366.1;
SEQUENCE 467 MA; 54402 MM; AFF16653590E6F68 CRC64;
                                                                                                                                                                                                                                                                                                                              EMBL; AE000751; AAC07560.1; -. Hypothetical protein; Complete SEQUENCE 480 AA; 55582 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeck R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.W., Olaon G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor suppressor pHyde.
                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 392:353-358(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V Match 50.3%; Score 96.5; Local Similarity 55.9%; Pred. No. 0. 1es 19; Conservative 6; Mismatche
                                                                                         10
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                                                                                                                                          RRSYR-----YKLLNWAYQ--QVQQNKEDAWIEHDVWRME 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRAHRYDLVNLAVKQVLANKSHLWVE-EVWRMEI
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                                                                                         RKTYRLKIPAKVSIDGKEYKVLDWSYEGFRIEKSKEDVFEKDKVYKVK 57
                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TYEMBLYE1. 07, Created)
(TYEMBLYE1. 07, Last sequence update)
(TYEMBLYE1. 20, Last annotation update)
uprotein AQ_1687.
                                                                                                                                                                                                            Conservative
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Primates;
                                                                                                                                                                                                                                    32.6%;
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Last annotation update)
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                                                                                                                                                                                                   Pred. No. 4;
7; Mismatches
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6; Mismatches
                                                                                                                                                                                                                                        Score 62.5;
Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                      proteome.
7BED49517A218046 CRC64;
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OSSOC7:
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
PULELIVE TRP homologous c
LTRPC4/CED-11.
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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Evans P.C., Coadwell W.J., Kilshaw P.J.;
"Inolation of a novel murine gene, Cezanne 2.";
"Inolation of a novel murine BMBL/GenBank/DDBJ d
EMBL; Auf 10384; CAN23048; 1) -.
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01-JUN-2002 (TrEMBLrel.
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"Isolation of a novel human gene, Cezanne 2.";
Sbmitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL, AM43033; CAD23047.1;
"EMBL, AM43033; CAD23047.1;"
EMBL/BAGSCE 928 AB; 100676 MM; 6E4623C2EB2C8058 CRC64;
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01-JUN-2002 (TrEMBLrel.
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Bukaryota; Metazoa; Chordata;

Bukaryota; Eutheria; Rodentia;

Mammalia; Eutheria; Rodentia;

MCBI_TaxID=10090;
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CEZANNE 2.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
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Sciurognathi; Muridae; Murinae; Mus
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Search completed: March 26, 2003, 16:49:46 Job time: 37.5814 secs
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Matches 11
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Best Local Similarity 43.5%; Pred. No. 30;
Matches 10; Conservative 5; Mismatches
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InterPro; IPR00332; OTU.
InterPro; IPR00365; Znr A20;
SMART; SM00259; Znr A20; 1.
SROUENCE 850802; OTU; 1.
SEQUENCE 8580A; 9401 MW; A7D6B1D280C9387F CRC64;
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Q9NQ55;
01-OCT-2000 (TrEMBLrel. 15,
01-DCT-2000 (TrEMBLrel. 15,
01-DEC-2001 (TrEMBLrel. 19,
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"Cloning and functional expression of C. elegans TRP isofoxms.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ272503, CAC68152-1;
LinterPro; IPR002111; Cat_Channel_TrpL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Igolation and characterization of two novel A20-like proteins.";
Blochem. J. 357-637-632 (2001).
BMBL; AJ293573; CA89749.1; ...
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MEDLINE-21356309; PubMed=11463333;
Evans P.C. Taylor E.R., Coadwell J., Heyninck K., Beyaert R.,
Kilshaw P.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primatee; Catarrhini; Hominidae; Homo.
MSD_TaxID=9606;
[1]
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SEQUENCE FROM N.A.
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                                                                                                                                          249 WRWQQTQQNKESGLVYTEDEWQKE 272
                                                                                                                                                                                                                                                                            y Match 29.9%; Score 57.5; DB 4; Length 858; Iocal Similarity 45.8%; Bred. NO. 33; heb 11; Conservative 3; Mismatches 9; Indels
                                                                                                                                                                                     11 WAYQQVQQNKEDAWI-EHDVWRME 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyright
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
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AAB75315
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        Extracellular loop Gene 20 human sereted pro Human Sereted pro Human Strakel con Human STRAP-1 prot Human protein SEO P7899 maino acid s prostate cancer-as
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ABG41121	AAM31599	AAM18991	AAM71318	AAM58802	ABB23372	ABB38169	ABG25300	AAY58197	AAB02785	AAY58202	AAB49481	AAB49482	AAE02790	AAU10187	ABB83366	AAB93224	AAB85775	AAU04564	AAU10220	AAU76538	AAU80190	ABG61933	AAE02781 ·	AAU10188	AAE02841	AAU10189	AAU04565	AAY58195	AAY52589	ABB83365	AAB49483	AAM79829	AAW86309	AAE02780
Human peptide enco	#5636	Peptide #5425 enco	О	Human brain expres	<b>#5371</b>		Novel human diagno		Peptide 2 of human	Human STRAP-1 pept	Human p-HYDE. Hom	Human p-HYDE 40.	Extracellular loop	Human Six-Transmem	Human Tumour Suppr	Human protein sequ	Human drug metabol	Human G-protein co	Human Six-Transmem	Tumour-associated	Human PUMPCn prote	Prostate cancer-as	six tran				G-proted	Human STRAP-2 prot	prostat	Murine Tumour Supp		v		Human six transmem

### ALIGNMENTS

AAY58199 standard; peptide; 34 AA.

AAY58199;

14-MAR-2000 (first entry)

Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region

Serpentine transmembrane antigen of the prostate, STBAD-1, prostate transmembrane domain, type IIIa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; pancretic cancer; overian cancer; tumour antigen; immunisation; immune response; cellular; humoral; antigen; accine; antibody; detection; diagnosis; cellular; humoral; anticancer vaccine; antibody; detection; diagnosis; cellular; humoral; anticancer vaccine; antibody; detection; d prognosis; monitoring; susceptibility; therapeutic inhibitor; targetting; recombinant protein.

Homo sapiens Synthetic.

W09962941-A2

01-JUN-1999; 09-DEC-1999 99WO-US12157.

TAYSOLT ANYSOLT UROG-) UROGENESYS INC. (AFAR/) AFAR D B. (HUBE/) HUBERT R S.

30-JUN-1998; 01-JUN-1998;

98US-0087520 98US-0091183

P789P protei

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AAE02787
ID AAE0
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XX Ext)
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Human; cytostatic; antiproliferative; vaccine; gene therapy; six transmembrane epithelial antigen of the prostate-1, STEAP-1; chromosome 'p22.3; cancer; prostate; colon; bladder; pancreatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 22; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LEON/)
                                                                               Extracellular loop #2 of human STEAP-1, suitable for cloning into
                                                                                                                                                              AAE02787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAY58198-Y58200 represent synthetic peptides that correspond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel proteins useful as diagnostic
                                                                                                                                                                                                  AAE02787 standard; peptide; 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     minimal side effects
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RAITANO A
SAFFRAN D
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ilarity 100.0%;
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Pred. No. 3.7e-19;
Wildmatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Length 34;
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WPI; 2001-367804/38
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                                                                                                                                                                                                                                                                                                                 07-JUN-2001
                                                                                                                                                                                                                                                                                                                                                     WO200140276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           ovarian; lung; extracellular loop; serpentine transmembrane antigen
  Example 19;
                                                       proceins,
                                                                         New STEAP
                                                                                                                                                                    Afar DEH,
                                                                                                                                                                                                          (UROG-) UROGENESYS INC
                                                       (six transmembrane epithelial antigen of the prostate) expressed in human cancers, useful for detecting and treating
                                                                                                                                                                    Hubert RS,
  Page 102;
                                                                                                                                                                                                                                             99US-0455486
187pp;
                                                                                                                                                                      Raitano AB,
  English
                                                                                                                                                                      Saffran DC,
                                                                                                                                                                      Mitchell SC,
                                                                                                                                                                         Faris
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The present invention relates to human six transmembrane epithelial Cantigue of the prostate (STEAP) protein. STEAP is a member of fell cartigue expentine transmembrane antigens. STEAP game is used in gene therapy. Inhibiting the development or progression of a cancer (eg. colon, bladder, lung, overlan and pancreatic) expressing STEAP (comprises administering a vaccine composition to the patient. Treating capture that a growth or killing cells expressing STEAP in a patient. Comprises administering a vaccine composition to the patient. Treating capture that expresses STEAP, or inhibiting growth or killing cells expressing STEAP (captures administering to the patient a capture that expressing STEAP, comprises administering to the patient a capture recording single chain monoclonal antibody that comprises the capture according single chain monoclonal antibody coding sequence to the cancer cells and that specifically binds to STEAP, such that the vaccor delivers the contracellularly. The present sequence is expressed and the encoded single chain monoclonal antibody is expressed contracellularly. The present sequence is expressed contracellularly. The present sequence is expressed and the present sequence is expressed. is located on chromosome 7p22.3

Sequence 34 AA;

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Matches
                                                           Query Match
                                                  Local
                   μ
              RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                       34;
                                                  Similarity
                                        Conservative
                                                 100.0%;
                                        0,
                                       Score 192; DB 22;
Pred. No. 3.7e-19;
; Mismatches 0;
                                                           Length
                                                             34;
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AAB75314 standard; Protein; 129

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03-APR-2001 (first entry

Gene 20 human secreted protein homologous amino acid sequence #133.

Human; immunosuppressive; antiarthritic; antirheumatic; nootropic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; neuroprotective; antiproliferative; antipateerial; virucide; fungicide; opthalmalogical; vulnerary; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; rifection; nervous system disorder; ocular disorder; chemotaxis; food additive;

secreted

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RESULT 4
AAB75315
ID AAB7
XX AAB7
XC AAB7
XC AAB7
XC AAB7
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XX Huma
KW Anti
KW neur
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Human; immunosuppressive; antiarthritic, antirheumatic; nootropic;
antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
                                                                                                                                                                                                                                       03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                         AAB75315 standard; Protein;
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(ROSE/) ROSEN C A.
                                                                                                                                                 Human secreted protein sequence encoded by gene 20 SEQ ID NO:134.
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This invention relates to polymucleotide sequences AAP3789 - AAP8386 CC which encode human secreted proteins AAP3260 - AAP3297. Included in the cirvention are protein sequences AAP3288 - AAB3341 which are reguences are represented proteins and secreted proteins and sequences with which these coff the secreted proteins and amazon acid sequences with which these coff the proteins share homology. Examples of the activities of the proteins and polymucleotides and the activities of the proteins and complymucleotides and the activities of the proteins and antagonists of the protein and polymucleotide (continuous) and vulnerary activity. The protein and polymucleotide (continuous) and vulnerary activity. The protein and polymucleotide (continuous) and vulnerary activity. The protein and polymucleotide (continuous) and vulnerary activity. The protein and polymucleotide (continuous) and vulnerary activity. The protein and polymucleotide (continuous) and vulnerary activity. The protein and polymucleotide (continuous) and vulnerary activity. The protein and polymucleotide (continuous) and the protein antagonists may be useful for treating, correcting and diagnosing diseases and disorders such as autoimmen (continuous) and the protein disorders of the continuous protein (continuous) and protein (continuous) and protein continuous antagonists and the sequences of the invention are continuous and continuous and continuous and peptide AAP5239 which are used (continuous) and continuous continuous and continuous continuous continuous and continuous continuous and peptide AAP5239 which are used (continuous) and continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continuous continu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 53-54; 530pp; English.
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ilarity 100.0%;
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Sorpentine transmembrane antigen of the prostate; STRAP-1, prostate; rransmembrane domain; type Illa membrane protein; expression; cencer; prostate cancer; bladder cancer; colon cencer; percette cancer; brownian cancer; bunder antigen; immunisation; immune response; estimate cancer; cellular; humoral; anticancer reactine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor; drug cargetting; recombiant procesin.
This sequence represents a novel human protein, STRAP-1 (serpentine transmembrane antigen of the proteins (ARSE) the prototype member of the STRAP family of proteins (ARSE)9-YES197) which exhibit a high degree of structural commercation, but which no significant structural homology to known human proteins. The STRA no significant structural homology to known human proteins.
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                                                       Claim 1; Fig 1A; 83pp; English
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                                                                                   proteins useful as diagnostic markers and therapeutic targets,
                                                                                                                                                 LEONG K.
RAITANO A B.
SAFFRAN D C.
                                                                                                      AAZ49395,
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HUBERT R S.
                                                                                                                                                                                                UROGENESYS INC.
                                                                                                                               Hubert RS,
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                                                                                                                                 Leong K,
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13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
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09-MAY-2000;
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                                             (CORI-) CORIXA CORP
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Matches
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                                                                                                                 27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; munnomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                    Human protein SEQ ID NO 1507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Fanger GR, Retter MW, Stolk DA, Day CH, Vedvick TS,
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
         Tang
Zhao
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM78845
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                                                                                                                                                                           03-FEB-2000;
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                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                             WO200157190-A2
                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                  (HYSE-) HYSEQ INC
                                                                                                        15-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer -
         84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 549; 579pp; English
       Liu C,
Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA;
                                                                           2000US-0496914.
2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0654936.
2000US-0653925.
2000US-0728422.
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ilarity 100.0%;
Conservative
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       Drmanac RT, Asundi
Wang J, Zhang J,
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Pred. No. 5.1e-18;
       Asundi V, Zhou P, nang J, Ren F, Chen
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       Xu C, Ca
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Carter D;
Cao.
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AAM01282
ID AAM
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                Kalos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polymucleorides (AAKS1456-AAKS145) and the encoded polypeptides (AAWB823-AAWB8020); that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polymucleorides and polypeptides are useful in gene therapy, vaccines or peride therapy. The polypeptides are useful in gene therapy activities, e.g., stem cell growth factor activity, haematopolasis regulating thind activity, insue growth factor activity, immunomobilatory activity and activity, insue growth factor activity. Immunomobilatory activity and activity, insue growth factor activity, immunomobilatory activity and activity, insue growth factor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a for use in vaccines -
                                                                                                                                                                                                                                                                                                                                                           cytostatic; gene therapy; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                  P789P amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Page 3800-3801; 6221pp; English
                       Claim 2, Page 510-512; 543pp; English
                                                                                                        WPI; 2001-425873/45.
                                                                                                                                 Wang
                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                    14-JAN-2000; 2000US-0483672
                                                                                                                                                                                                                                             16-JAN-2001; 2001WO-US01574.
                                                                                                                                                                                                                                                                          19-JUL-2001
                                                                                                                                                                                                                                                                                                     WO200151633-A2
                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; prostate-specific; diagnosis; vaccine;
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                                                                                                                               , Dillon DC, Mitcham
s MD, Fanger GR, Day
A, Meagher MJ;
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Pred. No. 5.1e-18
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Retter MW, Stolk
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olk JA, Skeiky
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Length 339; Indels

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RESULT 9
ABG61813
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Matches 34; Conserv
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08-DEC-2000;
08-DEC-2000;
24-JAN-2001;
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   The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method
                                                                                                                Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate tissue
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                                                                        Claim 27; Page 312; 436pp; English.
                                                                                                                                                                                                                                             N-PSDB;
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2000US-0733288
2000US-0733742
2001US-0733742
2001US-263957P
2001US-276791P
2001US-276791P
2001US-27898P
2001US-283922P
2001US-0847046
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Pred. No. 5.1e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprises contacting a biological sample from the patient with profestate cancer-associated polynuclectides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynuclectide sequences are differentially expressed in prostate typolynuclectide sequences constant are derived from the tissues of in prostate cancer and are derived from the tissues of various or prostate cancer and are derived from the tissues of various or crganisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for disgnosing and treating prostate cancer associated genes are useful for disgnosing or treating prostate cancer, as well as for useful for disgnosing or treating prostate cancer associated genes are useful for disgnosing or treating prostate cancer associated genes are useful for disgnosing as vaccine or in antisense applications.

20 in gene therapy, as a vaccine or in antisense applications.

21 ABG61800-ABG61944 represent prostate cancer-associated proteins.
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27-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RRSYRYKLLNWAYQOVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
   XU J.
DILLON D C.
MITCHAM J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 AA;
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                     2000US-0483672.
2000US-0536857.
2000US-05368100.
2000US-0577737.
2000US-0597793.
2000US-0597793.
2000US-065783.
2000US-0651236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                          2000US-0657279
2000US-0679426
                                                                                                                                                                                                                                                                                                                                                                    99US-0443686.
                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0232149.
99US-0288946.
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Pred. No. 5.1e-18;
Mismatches 0;
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Best Local (
                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                            The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cencers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                     Region
                                                                                                                                      Human, cytostatic; antiproliferative; vaccine; gene therapy; slx transmembrane epithelial antigen of the prostate-1; STEAP-1; chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                       06-AUG-2001
                                                                                                                                                                                                        AAE02780;
                                                                                                                                                                                                                      AAE02780 standard;
                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; SEQ ID NO 879; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                      progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                            diseases, in particular prostate cancer, and as markers for the
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI, 2002-255649/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Χu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SKEI/)
(HEPL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CART/)
(LISX/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RETT/)
(STOL/)
(DAYC/)
(VEDV/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KALO/)
                        Region
                                        Domain
                                                        Region
                                                                        Domain
                                                                                                               Homo sapiens.
                                                                                                                               pancreatic.
                                                                                                                                                                       Human six transmembrane epithelial antigen of prostate (STEAP)-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     New prostate-specific polynucleotides for diagnosing and treating
         Domain
                                                                                                                                                                                                                                                              185 RRSYRYKLLNWAYOQVQQNKEDAWIEHDVWRMEI 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (WANG/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JIAN/
                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                        1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JIANG Y.
KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RETTER M W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HARLOCKER S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARTER D.
                                                                                                                                                                                                                                                                                                                              339 AA;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                      (first entry)
                        /label= 1
158..166
         /label= HLA-A2_binding_peptide #5
163.,184
                                                               /label= Transmembrane_domain #1
                                                                       /label= Immunogenic_peptide #1 70..91
                                                                                       Location/Qualifiers
/label= Transmembrane_domain #3
                                               /label= HLA-A2_binding_peptide #2
                                                                                                                                                                                                                      Protein; 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŗ
                                                                                                                                                                                                                                                                                               100.0%; Score 192; DB 23;
100.0%; Pred. No. 5.1e-18;
ive 0; Mismatches 0;
                               = Transmembrane_domain #2
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                                                                                                                                                                                                                                                                                               Indels
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Carter D;
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                                                                                                                                                                                                                                                                                                Gaps
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 RESULT 12
AAW86309
ID AAW86
XX
AC AAW86
XX
DT 01-MA
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  01-MAR-1999
                                                                                                                                       Sequence
                AAW86309;
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New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and t
                                                                                                            WPI; 2001-367804/38
N-PSDB; AAD07067.
                                                                                                                                                                                                                                                         06-DEC-1999;
                                                                                                                                                                                                                                                                                            06-DEC-2000; 2000WO-US33040
                                                                                                                                                                                                                                                                                                                                  07-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                     WO200140276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
Example 2; Fig 1A-1B; 187pp; English.
                                                                                                                                                                   Jakobovits
                                                                                                                                                                                                                      UROGENESYS INC
                                                                                                                                                                 ۶
                                                                                                                                                                                  Hubert RS,
                                                                                                                                                                                                                                                         99US-0455486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Transmembrane_domain #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219..241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= HLA-A2_binding_peptide #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                302..310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Transmembrane_domain #6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= HLA-A2_binding_peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Transmembrane_domain #4
                                                                                                                                                                                                                                                                                                                                                                                                                                         label= HLA-A2_binding_peptide #4
                                                                                                                                                                                     Raitano
                                                                                                                                                                                                                                                                                                                                                                                                        "Encoded by TTGTAGAAT"
                                                                                                                                                                                  Æ,
                                                                                                                                                                                  Saffran DC,
                                                                                                                                                                                     Mitchell SC,
                                                       treating
                                                                                                                                                                                     Faris M
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The present sequence is human six transmembrane epithelial antigen of the prostate (STEAP)-1 protein of clone 10. STEAP is a member of cell surface serpentine transmembrane antigens. STEAP-1 gene is located on chromosome 7p2.2 and at used in gene therapy. Inhibiting the development or progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and pancreattle) expressing STEAP or inhibiting growth or killing cells expressing STEAP in a patient, comprises administering a veccine composition to the patient. Treating a patient with a cancer that expresses STEAP, or inhibiting growth or killing cells expressed administering to the patient is vector encoding single chain nonoclonal antibody that comprises the vector delivers the patient a vector encoding single chain in concording to the manoclonal antibody that specifically shinds to STEAP, such that the vector delivers the single chain monoclonal antibody coding equence to the cancer cells and the encoded single Chain monoclonal antibody coding that the spressed intracellularly.

Note: The present sequence is also shown in sequence listing of the specification, but it lacks amino acid residues at its N-terminal end.

(first entry)

375 AA;

375;

Gaps

Kidney injury associated molecule HW018 protein

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RESULT 13
AAM79829
ID AAM79
XX
AC AAM79
XX
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                                                                                                                                                                                                                                                              The present sequence represents a kidney injury associated molecule (KIM) procein. KIM proceins can be administered therapeutically (KIM) procein. KIM proceins can be administered therapeutically (KIM) procein. KIM proceins can be administered therapeutically consistent of the consistency of the c
                                                                                                                                                                                                 Matches
               AAM79829;
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 57-58; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kidney injury-associated molecule, KIM, polypeptides - upregulated in injured or regenerating tissues, useful to promote tissue growth and regeneration, especially to treat renal conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-045312/04.
N-PSDB; AAV80586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cate RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-1997;
23-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIM; tissue growth promotion; regeneration; renal condition; acute renal failure; acute nephritis; tumour.
                                               AAM79829 standard; Protein; 374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kidney injury associated molecule; kidney injury related molecule;
                                                                                                                                185
                                                                                                                                                                                                                                                                                             imageable KIM-binding reagent and imaging reagent accumulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BIOJ ) BIOGEN INC.
                                                                                                                                                             1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
                                                                                                                           RRSYRYKLLNWAYKOVOOSKEDAWVEHDVWRMEI 218
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hession CA,
                                                                                                                                                                                                                                                              339 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0047491.
97US-0047490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US10547
                                                                                                                                                                                                            94.8%;
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                                                                                                                                                                                                            Score 182; DB 20;
Pred. No. 1.2e-16;
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wei
                                                                                                                                                                                               0,
                                                                                                                                                                                                                            Length 339;
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03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-050875.
20-4UN-2000; 2000US-050875.
19-4UL-2000; 2000US-0620325.
01-SEP-2000; 2000US-064936.
15-SEP-2000; 2000US-063935.
20-MOV-2000; 2000US-063935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; namunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157190-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2001 (first entry)
(HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein SEQ ID NO 3475.
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WPI; 2001-476283/51. N-PSDB; AAK52962. Liu C, Wang D, Yang Y, Drmanac RT, Asundi V, Wang J, Zhang J, Re Wejhrman T, Goodrich Asundi V, Ren ch R, Zhou Chen ָט, , R & Wang ZW; Cao Y, Ma K

Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -

Claim 20; Page 350; 6221pp; English

The invention relates to polynucleotides (AAX51456-AAX53435) and the encoded polypeptides (AAX9333-AAX80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hasmatopoissis regulating activity, these growth factor activity, immunomodulatory activity and activity indictions of the control (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 inflammation. treatment of cancer, leukaemia, nervous system disorders, arthritis and

Sequence 374

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                    S
                                          Query Match
Best Local S
Matches 33
220 RRSYRYKLLNWAYQQVQQNKEDALIEHDVWRMEI 253
              RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                                            l Similarity
33; Conserv
                                             Conservative
                                                       93.2%;
                                                       Score 179; DB 22;
Pred. No. 3.3e-16;
                                             Mismatches
                                                                  Length 374;
                                               Indels
                                             0
                                             Gaps
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0

AAB49483 standard; Protein; 488

AAB49483;

08-MAR-2001 (first entry)

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RESULT 15
ABBB3365
ABBB3365
ABBB3367
AC ABBB33
AC ABBB33
AX O2-SE
XX Murin
AX Neuro
KW Neuro
KW Tumou
KW murin
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Matches
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29-APR-1999;
26-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present procein is rat p-HYDE. p-HYDE induces susceptibility of a cancer cell to cell death. The p-HYDE gene is associated with the regression of tumour growth in vivo, the induction to susceptibility to approval to the present of the prevention of susceptibility to open the prevention of approximation of approximation of the present of UV damage and the failure to repair DN. The present sequence may be used to reat concer, preferably melanoma, lymphoma, leukaemia, prostate,
                                                                                                                                                                                                                                                                                 Neuroprotective; cytostatic; TSAP6; apoptosis; cancer; neurodegeneration; Tumour Suppressor Activated Pathway 6; TSAP6 binding protein; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                   02-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 31; Page 20; 171pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-032016/04.
N-PSDB; AAC89167.
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                                                                                       04-JUL-2002.
                                                                                                                                                                                                     Mus musculus.
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                                                                                                                                                                                                                              Disclosure; Page 75-77; 79pp; French.
                                                                                                                                                                                                                                                                                                     N-PSDB; ABN85026.
                                                                                                                                   neurodegeneration.
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18-SEP-2001; 2001WO-FR02896
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364
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                1 RRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI 34
RRSHRYDLVNLAVKQVLANKSRLWVEEEVWRMEI
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1 REVIHPLATSHQQYFYKIPILV 22
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## SUMMARIES

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Mammalia, Eutheria;
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01-MAR-2001 (TrEMBLYel. 16, Last amotation update)
Six transmembrane endothelial antigen of PAEC.
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                      "Functional annotation of a full-length mouse cDNA collection.",
Nature 409:685-690(2001).
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.1%;
90.9%;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 108;
Pred. No.
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Q924J9;
                                                                                                                                                                                                                                         STRAIN=C57BL/6;
MEDLINE=21371909; PubMed=11479226;
MEDLINE=21371909; PubMed=11479226;
Yang D., Holt G.E., Velders M.P., Kwon
"Murine six-transmembrane epithelial ar
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SEQUENCE 339 AA; 39264 MW;
                                                                                                   transgenic adenocarcinoma mouse prostate mice.";
Cancer Res. 61:5857-5860(2001).
EMBL; AF297098; AAK83126.1; -.
                                                                                                                                                                                   Yang D., Holt G.E., Velders M.P., Kwon B.D., Kast W.M.; "Wurine six-transmembrane epithelial antigen of the prostate, prostate stem cell antigen, and prostate-specific membrane antigen; prostate-specific cell-surface antigens highly expressed in prostate cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Six-transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases EMBL, AY029584; AAK50537.1; - MGD; MGT:591578; 101000DDRRK.
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Mammalia; Eutheria;
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Mus musculus (Mouse)
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01-DEC-2001
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                          SEQUENCE
                                                     Transmembrane
                                                                            MGD; MGI:1917608; Steap.
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                          39318 MW;
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Last sequence update)
Last annotation updat
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Pred. No.
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Pred. No.
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Sciurognathi; Muridae; Murinae; Mus
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Sciurognathi;
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                          4B26A71FF559E84F CRC64;
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Best Local S
Matches 17
C STRAIN-SP370 / ATCC 700294 / SEROTYDE M1;

MEDILINE-2119684, Pubmed=1129696,

Perretti J.J., McShan M., Ajdic D.J., Savic D.J., Savic G.,

A Primeaux C., Sezate S., Suvcova A.M., Kenton S., Lai H.S., Lin

Qian Y., Jia H.G., Najar P.Z., Ren O., Zhu H., Song L., White

TYON T., Jia H.G., Najar P.Z., Ren O., Zhu H., Song L., White

TYON T., Jia H.G., Najar P.Z., Ren O., Zhu H., Song L., White

TOO Service genome equance of an M1 strain of Streptococcus pyo

TOO Natl. Acad Science of an M1 strain of Streptococcus pyo

RE INCEPTO, JERO01291, DAM, MITTANE.

RE INCEPTO, JERO0291, DAM, MITTANE.

RE INCEPTO, JERO0291, NA, MASS.

RE PERS. PERS. PROS. NA, MASS.

RE PERS. PERS. PROS. NA, MASS.
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Best Local Similarity
Matches 8; Conserv
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Q9A0P6
Q9A0P6
Q1-UN-2001 (TrEMBLrel. 17, Created)
Q1-UN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-UN-2001 (TrEMBLrel. 21, Last annotation update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Q1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Q2-UN-2004 (TremBlrel. 21, Last annotation update)
Q2-UN-2004 (TremBlrel. 21, Last annotation update)
Q3-UN-2004 (TremBlrel. 21, Last annotation update)
Q4-UN-2004 (TremBlrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ikebe T. Wada A., Inagaki Y., Sugama K., Tanaka D
Katsukawa C., Pujinaga Y., Abe Y., Watanbe H.;
"Complere sequence of temperate phage PhiNHH.1.",
Submitted (OCT-2001) to the BMBL/GenBank/DDBJ datal
InterPro. 11PR003115; ParBe.
Pfam: PF0215; PerBe.;
Pfam: PF0215; PerBe.;
Hypothetical procein.
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01-DEC-2001 (TrEMBLrel. 19, Cr.
01-DEC-2001 (TrEMBLrel. 19, La
01-MAR-2002 (TrEMBLrel. 20, La
Hypothetical 19.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
Bacteria; Firmicutes; Bacillus/Clostridium
Streptococcaceae; Streptococcus.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
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17, Conserv
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77.3%;
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1.9e-07;
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Lai H.S., Lin S.P
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Matches 8; Conserv
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Matches 8; Conser
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
EMBL, APS6232; AAM08128.1;
SEQUENCE 456 AA, 50430 MM
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01-JUN-2002
01-JUN-2002
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PRINTS; PR00506; DZINSMPTPRASE.

PRINTS; PR00506; SZINSMPTPASE.

SMART; BR00470; PATBc; 1.

PROSITE; P800092; N6 MTASE; UNKNOWN 1.

PROSITE; P800092; N6 Complete proteome.

SEQUENCE 388 AA; 43690 MM; 1258786206062827 CRC64;
                                                                                                                                                                                              SEQUENCE FROM N.A.
Steiner M.S., Allay J.A., Wang C.;
YA novel prostate-derived tumor suppressor ";
YA novel prostate-derived tumor suppressor ";
Submitted (FERS-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF23864; AL172266.1;
                                                                                                                                                                                                                                                                                                                                          01.-UNV-2002 (TEEMBLER). 21, Created)
01.-UNV-2002 (TEEMBLER). 21, Last sequence update)
01.-UNV-2002 (TEEMBLER). 21, Last annotation update)
Tumor suppressor pHyde.
Themos sappiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria;
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      RDVLQPYVQESQNKFFKLPVSV 254
                                             REVIHPLATSHOOYFYKIPILV
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Pred. No.
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Pred. No.
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01-OCT-2000
01-OCT-2000
01-DEC-2001
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Q9QAP4;
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                          Robert S.; Robert S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Ros C. Belk S.; Robert S.; R
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01-0CT-2000 (TERMBLrel. 15, Last sequence update)
01-0CC-2000 (TERMBLrel. 19, Last annotation update)
CDNA FLJ10829 fis, clone NT2RP4001139 (DUALIN 2).
Homo sepiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yaubourdolle M., Kellermann O., Loric S.;
"Dudulin 2. a new tumor antigen expressed in various human tumors.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO01581, BAA91839.1,1 ...
EMBL, AY025585, AXC5638.1,1 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Studikawa T., Nagai K., Sugano S., Aotsuka S., Yoshikawa Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Nakamura Y., Nagahari K., Masuho Y., Sasaki N., "NEDO human cDNA sequencing project.",
Submitted (FEB-2000) to the EMEL/GenBank/DDBJ databases.
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Mammalia; Eutheria;
alphaherpesviruses.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL, AF078729; AAA6115.2;
SEQUENCE 929 AA; 100755 MW; BC0E569F9Z230E
                                                                                                                                                                           STRAIN-BANFFSHIRE 82;
ROB C., Belak S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BANFFSHIRE 82;
MEDLINE=99221732; PubMed=10203465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, Alphaherpesvirinae.
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cervid herpesvirus 1.
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PROSITE; PS00290; IG_MHC; UNKN
SEQUENCE 488 AA; 54616 MW;
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                                                                                                                                      "Characterization of the glycoprotein B gene from ruminant
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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(TrEMBLrel.
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Pred. No.
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Aotsuka S., Yoshikawa Y.,
Aotsuka S., Yamamoto J., Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Nouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II, Bræssicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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EMBL; ACOO G61; AAD32790.1; -
ITREOEPTO; IFRO0345; CytC heme bind.
PROSITE; PSO0190; CYTOCHEOME C; UNIX
SEQUENCE 233 AA; 26250 MM; 22661
   SEQUENCE FROM N.A.
STRAIN=MB4T / JCM11007;
                                                                                               Thermoanaerobacter tengoongenala.
Bacteria, Pirmicutes, Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
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AT2G37810.
                                                                      NCBI_TaxID=119072;
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HAL OR VNG24216.
HALObacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriacae; Halobacterium.
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Q9HMR3;
01-MAR-2001
01-MAR-2001
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Bao Q., Tian Y. Li M., Xu Z., Xuan Z., Hu S., Dong W., Yang J. Chen Y., Xue Y., Xu Y., Lia X., Huan L., Dong X., Ma Y., Ling Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:699-70(2002).

EMBLY, ABC13162, AAMC314.1; -.
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SEQUENCE 427 AA; 46642 MW; 0A4E1F2796CEE4AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome.
SEQUENCE 431 AA;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Local Similarity 72.7%;
les 8; Conservative
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Pred. No.
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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DNA Res. 7347-355(200).

DNA Res. 7347-355(200).

ENHI, ABOSISO0: BAR21804.1;
InterPro: IPRO0290; P 746h extensm.
PRINTS: PRO1471; HISTANIEMSR.
PRINTS: PRO1471; HISTANIEMSR.
PRINTS: PRO1471; HISTANIEMSR.
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Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., Ohara O.;
*Prediction of the coding sequences of unidentified human genes. XIX.
The complete sequences of 100 new cDNA clones from brain which code
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46 TSHRQQFYQMPV 15:
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Similarity 58.3%;
7; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
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Match Length
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Gapop 10.0 ,
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(without alignments)
168:726 Million cell updates/sec
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(c) 1993 - 2003 Compugen Ltd.
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                                     T46025
AG3323
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        probable type II p
hypothetical prote
glycoprotein gI pr
glycoprotein gI pr
isoleucyl-tRNA syn
                                                                                   hypothetical prote
hypothetical prote
penicillin-binding
sperm motility inh
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peptide methionine
cytochrome f - red
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                                                                                                                                                                                                                hypothetical prote
nucleoporin homolo
                                             hypothetical prote
hypothetical prote
probable type II p
                                                                          sperm motility inh
DNA-directed RNA p
                                                                                                                adenylate cyclase hypothetical prot
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                                                                                                                                             probable membrane
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O-acetylhomoserine
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                                                                                                                                                                                                                                            hypothetical prote
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hypothetical coi	2 T37550	485	37.1	43	•
O-acetylhomoserine	2 T44655	442	37.1	43	
cysteine synthase	2 AH3397	434	37.1	43	_
O-acetylhomoserine	2 D72324	430	37.1	43	
O-acetylhomoserine	2 A86634	426	37.1	43	•
hypothetical	2 T16447	385	37.1	43	_
oxaloacetate decar	2 B72324	384	37.1	43	_
transcription regu	2 C86873	379	37.1	43	_
exte	2 896798	373	37.1	43	
probable aspartate	2 882118	338	37.1	43	
aspartate-semialde	1 S14523	337	37.1	43	
Hypothetical	2 F86319	336	37.1	43	
hypothetical	2 F83356	295	37.1	43	
extensin	2 871227	284	37.1	43	
hypothetical	2 G86128	326	37.5	43.5	
hypothetical	2 D91287	326	37.5	43.5	

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R.Ng. W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Lekthauser, B.; Kelter, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
Jung, K.H.; Alam, M.; Freitas, T. 12.76-12181, 2000
A; Authbors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lie
A; Title: Genome sequence of Halbacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: G8473
A; Scatus: preliminary
A; Molecule type: DNA
A; Residues: 1-177 cSTO-
A; Cross-references: GB:AE004437; NID:g10580713; PIDN:AAG19555.1; GSPDB:GN00138
C; Superfamily: peptide methionine sulfoxide reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein H10021 - Haemophilus influenzae (strain Rd Kw20)
(;Species: Haemophilus influenzae
(;Species: Haemophilus influenzae
(;Species: Nap.1995 Heequence_rvision 18-Aug-1995 #text_change 08-Oct-1999
(;Accession: E64140
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
(Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.D.; Hormann, J.L.; Geoghagen, N.S.M.
(D.M.; Brandon, R.C.; Fine, L.D.; Frickhann, J.L.; Hormann, J.L.; Geoghagen, N.S.M.
Rociance 269, 496-512, 1995
A;Authors: Gnehm, C.L.; KcDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Authors: Gnehm, C.L.; KcDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Reference number: A64000; MUID:95350630; PMID:7542800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.NStatus: nucleic acid sequence not shown; translation not shown
A.Notecule type: DNA
A.Pocidues: 1-416 (TICR)
A.Pocidues: 1-416 (TICR)
A.Cores-references: GB:U32687, GB:L42023, NID:g1572955, PIDN:AAC21699.1, PID:g1572965, TI
A.Note: best homolog was a hypothetical protein from Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide methionine sulfoxide reductase [imported] - Halobacterium sp. NRC-1
C.Species; Halobacterium sp. NRC-1
C.pate: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 16-Peb-2001
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Best Local S
Matches 10
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Pred. No. 1
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Cibete: 19-Mer-1957 Heequence_revision 09-May-1997 #text_change 11-Jun-1999 CiAccession: 873186 Applicable of the Porphyra purpurea chloroplast genome. Firstle: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome. A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 873108 A;Reference number: 87310 CREI: A;Rote: the nucleotide sequence was submitted to the EMBL Data Library, October 1995 A;Cene: petA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Genome: chloroplast
C;Superfamily: cytoch
C;Keywords: chloropla
H84392
                    RESULT 5
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                                                                                                                             S
                                                                                                                                                     Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-233 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                            A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
A.Reference number: A84420; MUID:20083487; PMID:10617197
A.Accession: D84797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, L.; ouss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, White, 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein At2g37810 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (nouse-ear cress) C;Dates: 02-Feb-2001 Heat_Colares (20-Feb-2001 Heat_Colares) C;Accession: D84797
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C.Species: chloroplast Porphyra purpurea
C.Date: 19-Mar.197 #sequence_revision 09-May-1997 #text_change 11-Jun-1999
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Matches
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Best Local
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position: 2
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Local Similarity 40.7%;
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nes 9; Conservative
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                                                                                                                                4 IHPLATSHOOYFYKIP 19
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                                                                                                                                                                         Conservative
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Pred. No.
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Pred. No.
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Pred. No. 7.
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micleoporin homolog - fission yease (Schizosaccharomyces pombe) c;Specles: Schizosaccharomyces pombe c;Specles: Schizosaccharomyces pombe c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1997 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1997 #text_change c;Date: 03-Dec-1997 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_change c;Date: 03-Dec-1999 #text_c
A./Rolecule type: DNA
A./Residues : 1-75 < WOO.
A./Cross-references: EMBI:Al109846; PIDN:CAB52802.1; GSPDB:GN00067; SPDB:SPBC17G9.04c
A./EXPSCIAMENTAL BOURCE: Strain 972h-; COSMIG C17G9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Watches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.MoLecule type: DNA
A.Residues: 1-431 <STO-
A.Residues: 1-431 <STO-
A.Residues: GB:AE004437; NID:g10581828; PIDN:AAG20508.1; GSPDB:GN00138
C.Genetics:
A.Gene: hal
C.Superfamily: O-succinylhomoserine (thiol)-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T. 12.176-12181, 2010
Proc. Natl. Acad. Sci. U.S.A. 97, 12.176-12181, 2010
A;Authbras Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lit A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: H84392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: MIPS:YDR117c
A;Cross-references: SGD:S0002524
A;Map position: 4R
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 EILHPLLTNNFTEFYQI 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 2;
Pred. No. 12;
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A;Bacters preliminary
A;Btatus preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-296 «GLA»
A;Cross-references: GB:NC_003210; PIDN:CAC98911.1; PID:gl6410222; GSPDB:GN00177
A;Cross-references: GB:NC_003210; PIDN:CAC98911.1; PID:gl6410222; GSPDB:GN00177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exceinin homolog HRGP2 - soybean (fragment)
N,Alternate names: hydroxyproline-rich glycoprotein HRGP2
N,Alternate names: hydroxyproline-rich glycoprotein HRGP2
C,Debeis: 01yeise mac (moybean)
C,Debeis: 01yeise mac (moybean)
C,Debeis: 01yeise mac (moybean)
C,Debeis: 01yeise mac (moybean)
C,Debeis: 01yeise mac (moybean)
C,Debeis: 01yeise mac (moybean)
C,Riches: 1801a:101
A,Riche: 1801a:101
A,Robersioe mamber: 2.6058; MUD:0421312; pMID:8159793
                                                                                                                                                                                                                                                                                                                                                      D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
Science 294, 849-852, 2001
A.; Mulbors: Kreft, J.; Kuhn, H.; Kunst, F.; Kurspkat, G.; Madueno, B.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.;Title: Comparative genomics of Listeria species.
A.;Reference number: AB1077; MUID:21537279; PMID:11679669
A.;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.;Accession: AII178
C.;Accession: AII178
R.Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rzanscription regulator homolog lmo033 [imported] - Listeria monocytogenes (strain C;5pecies: Listeria monocytogenes (strain C;5pecies: 1steria monocytogenes (strain C;5pate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
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A; Map position: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-169 < HON>
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                                                                                            Query Match
Best Local S
Matches
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Best Local
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les 8; Conserva
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nes 7; Conserv
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   EILHELSSTHDCAFYRI 238
                                          EVIHPLATSHOOYFYKI 18
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l Similarity 57.1%;
8; Conservation
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                                                                                                                   39.7%;
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Pred. No.
                                                                                            6
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                                                                                                                   Pred. No. 11;
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Science 294, 484-982, 2001
Science 294, 484-982, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduenc
A; Authors: Kreft, J.; Kuhn, M.; Tierrez, A.; Vazquez-Boland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: Ab1077; MOID:21537279; PMID:11679669
A;Accession: Ab1508
phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain T22F8.180 [similarity] - Arabidopsis t
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Bate: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Marches 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                              A.Wolecule type: DNA
A.Residues: 1-425 «GLA»
A.Gross-references: GB.AL592022; PIDN:CAC95836.1; PID:g16413044; GSPDB:GN00178
A.Sxperimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O-acety/homoserine sulfnydrylase homolog lino604 (imported) - Listeria innocua
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
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C;Superfamily: O-succinylhomoserine (thiol)-lyase
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                                                                           T08576
                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
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                                                                                                  RESULT 12
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Best Local
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Buchrieser, C.; Amend, chaud, E.; Durand, L.;

Dussurget,

A.; Baquero, P.; Berche, P.; Dussurget, O.; Entian, K.D.; I

; Bloecker, Fsihi, H.;

(strain 2

G.; Madueno, E.; Maitournam, A.; Mai uez-Boland, J.A.; Voss, H.; Wehland,

Conservative 39.7%;

Mismatches Score 46; Pred. No.

BB 2

Length 425

Indels

0,

Gaps

0,

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Science 294, 484-852, 2001
Science 294, 849-852, 2001
A; Authors: Kreft, J; Kuhn, M; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Sinoes, N.; Tierrez, A.; Varquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
A;Telte: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1149
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C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-200:
C:Accession: AD1149
                                                                                                                                                                                                               C; Superfamily: O-succinylhomoserine (thiol) - lyase
                                                                                                                                                                                                                                                                                         A.F.Residues: 1-425 cGLA>
A.Cross-references: GBLVC_003210; PIDN:CAC98674.1; PID:g16409971; GSPDB:GN00177
A.Experimental source: strain EGD-e
                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
376 IIHPASTTHQQ 386
                                                   3 VIHPLATSHOO 13
                                                                                                                                                                                                                                            1mo0595
                                                                                                   Similarity
7; Conserv
                                                                                                       Conservative
                                                                                                                                 39.7%;
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Pred. No.
                                                                                                           Mismatches
                                                                                                                                     DB
17;
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Fsihi, H.;
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R.Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Puji, F.; Hir: Nucleic Acids Res. 28, 417-431, 2000

Nucleic Acids Res. 28, 417-431, 2000

A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A,Reference number: A83650; MUID:20512582; PMID:11058132

A,Accession: C8375
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A.Introns: 49/3, 91/3, 121/3; 140/3; 179/2; 186/3; 213/1; 241/2; 273/3; 306/1; 330/1;
C;Superfamily: yeast cytosolic phenylalanine-tRNA ligase beta chain
C;Keywords: aminoacyi-tRNA synthecase; ligase; protein blosynthesis
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A.Experimental source: cultivar Columbia; BAC clone T22F8
C.Genetics:
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R.Jervan, M., Zimmermann, W., Grueneisen, A., Wambutt, R., Bancroft, I., Mewes, H.W., May submitted to the Protein Sequence Database, May 1999
A,Reference number: Z16442
A,Accession: T0876.
                        A;Cross-references:
C;Genetics:
                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-735 <KUR>
                                                                                                                                                                     A./Title: Genome sequence of Yersinia postis, the causative agent of plague
A.Reference number: AB0001, MUID:21470413; PMID:11586360
A.Accession: AD0341
                                                                                                                                                                                                                                                             R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillimgworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Ritherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable membrane protein YPO2801 [imported] - Yersinia pestis (strain CO92)
C.Species: Yersinia pestis
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Crose-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06322.1; GSPDB:GN00
A)Experimental source: strain C-125
C;Genetigs:
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A; Residues: 1-428 <BEV>
A;Gene: YPO2801
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                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Yersinia pestis
;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                         Accession:
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Best Local Similarity 63.6%;
Matches 7; Conservative
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nes 7; Conservativo
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                                                     GB:AL590842; PIDN:CAC93035.1; PID:g15980773; GSPDB:GN00175

 Mismatches

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Pred. No. 17;
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Job time : 14.5349 secs
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2003,

16:50:38

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Query Match
Best Local Similarity
Tarches 7; Conserve
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A;Autthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome (A,PatGerence number: A70500; MUID:9925997; PMID:9544230

A;Bactus; preliminary, nucleic acid sequence not shown; translation not shown A;Molecule type: DNA, Accession: 1707 COL-
A;Status; preliminary, nucleic acid sequence not shown; translation not shown A;Molecule type: DNA, A;Coossion: CR01-2001, GB:A122456; NID:93261576; PIDN:CAA98091.1; PID:e245021; i
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                                                                                                                                                                                        A, Experimental source: strain H37Rv C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein Rv1327c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C.Dates: 17-ul-1998 #eequence_revision 17-ul-1998 #text_change 22-Oct-1999 C;Accession: C70770
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Best Local Similarity
Matches 10; Conserv
389 HPWAREHROWFTELP 403
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Pred. No.
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                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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116
1 REVIHPLATSHQQYF
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339	339	339	339	339	104	104	104	22	22	Match Length DB	
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ABG61813	AAM01282	AAM78845	AAU69927	AAY58194	ABG43832	AAM73944	ABB40417	AAE02786	AAY58198	Length DB ID	
Prostate cancer-as	P789P amino acid s	Human protein SEQ	Human prostate cDN	Human STRAP-1 prot	Human peptide enco	Human bone marrow	Peptide #7923 enco	Extracellular loop	Human STRAP-1 pept	Description	

Drosophila melanog	ABB59692	22	1176	38.4	44.5
Drosophila melanog	ABB69782	22	151		45
Novel human diagno	ABG08176	22	146	38.8	45
Murine Tumour Supp	ABB83365	23	526	39.7	46
Rat p-HYDE. Rattu	AAB49483	22	488	39.7	46
Listeria monocytog	ABB48993	23	425	39.7	46
Listeria monocytog	ABB47546	23	296	39.7	46
Staphylococcus epi	ABP38703	23	195	39.7	46
Human Tumour Suppr	ABB83366	23	488	41.4	48
Human protein sequ	AAB93224	22	488	41.4	48
Human drug metabol	AAB85775	22	488	41.4	48
Human G-protein co	AAU04564	22	488	41.4	48
Human Six-Transmem	AAU10220	22	488	41.4	48
Human p-HYDE. Hom	AAB49481	22	487	41.4	48
Human p-HYDE 40.	AAB49482	22	456	41.4	48
Streptococcus poly	ABP29233	23	388	41.4	48
Human G-protein co	AAU04565	22	237	41.4	48
	AAO10072	22	128	42.2	49
_	ABG00113	22	1273	58.6	68
	ABG12306	22	576	-	68
Human Six-Transmem	AAU10187	22	490		83
Tumour-associated	AAU76538	23	454	58.6	68
Human PUMPCn prote	AAU80190	23	454	58.6	68
Prostate cancer-as	ABG61933	23	454		68
Human six transmem	AAE02781	22	454	58.6	68
	AAU10188	22	454		68
Human STEAP-2 prot	AAE02841	22	450	58.6	68
	AAU10189	22	419	58.6	68
llular	AAE02789	22	26	58.6	68
Kidney injury asso	AAW86309	20	339		89
Human 5' EST secre	AAY12304	20	109	79.3	92
Human 5' EST secre	AAY11840	20	95	83.6	97
Human six transmem	AAE02780	22	375		116
-	AAM79829	22	374	100.0	116
Human P789P protei	ABB95387	23	339	100.0	116

## ALIGNMENTS

AAY58198	58198	ULT 1
standard;		
peptide;		
22		

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AAY58198;

Human STRAP-1 peptide, corresponding to STRAP-1 extracellular region 14-MAR-2000 (first entry)

Serpentine transmembrane antigen of the prostate; STRAP-1, prostate; transmembrane domain; type III a membrane protein; expression; cancer; prostate cencer; hladder cancer; colon cancer; patereatic cancer; overlan cancer; tumour antigen; immunisation; immune response; callular; humoral; anticancer vaccime; antibody; detection; diagnosis; prognosis; monitoring; succeptibility; therapeutic inhibitor; drug cargeting; recombinant protein.

Homo sapiens Synthetic.

W09962941-A2

01-JUN-1998; 30-JUN-1998; 01-JUN-1999; 09-DEC-1999. (UROG-) UROGENESYS INC. (AFAR/) AFAR D E. (HUBE/) HUBERT R S. 98US-0087520. 98US-0091183. 99WO-US12157

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                                                                                                                                                                                                                                                                                                                                                 member of the STRAP Early of proteins (ANSES) - VESSON which show members of the STRAP is not been considered as the structural conservation, but which show consistent a high degree of structural conservation, but which show consistent and the structural conservation, but which show consistent and the structural conservation, but which show consistent and the structural conservation, but which show consistent and the structural conservation is thought to be a cype illa membrane protein and is expressed predominantly in proteate cells in normal human tissues. Structurally, STRAP-1 is a 33 maino call protein characterised by six transmembrane domains and intracellular N and creating the six transmembrane domains and conservation and protein expression is maintained at high levels and throughout all steages of protein expression is maintained at high levels and conservation and protein structurally strain cancer. STRAP-1 mRNA and/or protein is called oversexpressed in certain other cancers, including bladder, colon, cancer the function of the STRAP proteins is not known. They may be ion channels of the strain content of the STRAP proteins is not known. They may be ion channels of the strain content of the STRAP-1 and STRAP-1 and STRAP-2 are cell-nurface tunnor antigens. Immunication with a STRAP protein induces cellular and humoral immune responses against competition induces cellular and humoral immune responses and to generate pectific binding agents, to produce anticancer vaccines and to generate competition of strap protein may be used for detection, prognosis, and monitoring of cancers (or succeptibility to cancer), as therapeutic specific and propostic reagents for identifying STRAP-spressing cells strap strap content protein are expressed mainly consistent and expressed mainly consistent and expressed mainly consistent and expressed mainly consistent on their tissues.
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Matches 22
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(RAIT/)
(SAFF/)
Human; cytostatic; antiproliferative; vaccine, gene therap;
six transmembrane epithelial antigen of the prostate-1; STEAP-1;
chromosome 7p22.3; cancer; prostate; colon; bladder; pancreatic; lung;
                                                                                           06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AN75819-Y58200 represent synthetic peptides that correspond to the extracellular regions of STRAP-1 (serpentine transmembrane antigen of the prostate, AN758194). These peptides were used to raise monoclonal anti-STRAP-1 antibodies. STRAP-1 is the prototype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel proteins useful as diagnostic markers and therapeutic targets, particularly for prostatic cancer -
                                                          Extracellular loop #1 of human STEAP-1, suitable for cloning into pfc.
                                                                                                                                                 AAE02786 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                              minimal side effects on other tissues.
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SAFFRAN D C.
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                                                                                                                                                                                                                                                                                                                  DB 21; Length 22;
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04-FEB-2002 (first entry

ABB40417 standard; Peptide; 104

Local

22; Similarity

Conservative

0

0

0

Gaps

0

100.01;

Score 116; DB 2 Pred. No. 7e-12; Mismatches

Length

1 REVIHPLATSHOQYFYKIPILV 22 REVIHPLATSHOQYFYKIPILV 22

Human; foetal liver; gene expression; single exon nucleic acid probe. Peptide #7923 encoded by human foetal liver single exon probe

30-JAN-2001; 2001WO-US00669

09-AUG-2001 WO200157277-A2

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The present invention relates to human six transmembrane epithelial CC satisfies of the proseste (SYEAP) protesh. SYEAP is a member of cell CC satisfies expentine transmembrane antispens. SYEAP gene is used in gene therapy. Inhibiting the development or progression of a cancer (eg. CC prostate, colon, bladder, lung, overian and pancreatic) expressing SYEAP comprises administering to the state of the patient. Treating comprises administering a vaccine composition to the patient. Treating comprises administering to the patient a vector encoding single chain monoclonal antibody that comprises the craft vector encoding single chain monoclonal antibody that comprises the trait specifically binds to SYEAP, such that the vector delivers the cancer cells and comprises the single chain monoclonal antibody coding sequence to the cancer cells and continuous chain monoclonal antibody is expressed intracellularly. The present sequence to the cancer cells and continuous coding into pEr, which is used in the invention. SYEAP-1 comprises is located on chromosome 7p22.3.
                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proceins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New STEAP (six transmembrane epithelial antigen of the prostate) proteins, expressed in human cancers, useful for detecting and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ovarian; extracellular loop; serpentine transmembrane antigen
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                                                                          22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0455486
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DB 22;
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AMT3914 4

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26-MAY-2000; 2000US-0274756

30-JUN-2000; 2000US-0608408

03-AUG-2000; 2000US-0608408

13-SEP-2000; 2000US-0334687

27-SEP-2000; 2000US-0336539

04-CCT-2000; 2000US-0336539
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
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Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-483447/52.
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27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                              09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human bone marrow expressed probe encoded protein SEQ ID NO:
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    Penn
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                                                              (MOLE-)
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    SG,
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                                                              MOLECULAR DYNAMICS INC.
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Hanzel DK,
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2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-02343697.
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ilarity 100.0%;
Conservative 0;
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    Chen W,
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Pred. No. 3.8e-11;
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    AB648832 5 AB648832 5 AB64883 5 AB64883 5 AB6488 5 AB648 5 AB6
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Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histicoytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;

Homo sapiens.

hyaline membrane

disease.

Human; single exon probe; asthma; lung cancer; CODD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis, neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

Human peptide encoded by genome-derived single exon probe

SEQ ID 33497

04-FEB-2000; 2000US-180132P 26-MAY-2000; 2000US-07456P 30-JUN-2000; 2000US-06084408. 03-MUS-2000; 2000US-0512366 21-SEB-2000; 2000US-214657P 27-SEB-2000; 2000US-216339P 04-CCT-2000; 2000US-216339P

30-JAN-2001, 2001WO-US00665

15-NOV-2001 WO200186003-A2

Claim

27;

SEQ

ij

No 33497; 634pp; English

measure gene expression in

Spatially-addressable set of single exon nucleic acid probes, used

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human lung samples

Penn

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Hanzel DK,

Chen W,

Rank DR;

(MOLE-)

MOLECULAR DYNAMICS INC

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                                                                                                                                                                                                                                                          probes which are derived from genomic sequences expressed in the human
bone marrow. They can be used to measure gene expression in bone marrow
samples, which may enable the improved diagnosis and treatment of cancers
such as lymphoma, leukaemia and myeloma. The present sequence is a
protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
 19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 34250; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                       analyzing gene expression in human bone marrow
                                                       ABG43832
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                                                                                                                                                                                             Local
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                                                   standard; Peptide; 104 AA
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ilarity 100.0%;
Conservative C
                                                                                                                                                                                                                                                                                                                                   invention
(first entry
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                                                                                                                                                                                             Score 116; DB
Pred. No. 3.8e-
                                                                                                                                                                                  Mismatches
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-11;
0;
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mucleic said expressed in those many in measuring gain expression in a market settle expression in a market settle expression in a callection of detectably babeled nucleic acids derived from human lung.

C mark, and (b) measuring the label detectably bound to each probe of the array identifying exons in a eakryotic genome, comprising of the extrayotic genome, comprising of the extrayote, and (b) detecting at least one exon from genomic sequences of the extrayote and (b) detecting genome, comprising the labeled nucleic acids from eakryotic lung mRN, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; masigning exons to a single exon probe (comprising (a) identifying exons from genomic sequence by the method (comprising (a) identifying exons from genomic sequence by the method (comprising (a) identifying exons from genomic sequence by the expression of the exons in the tissues and/or cell types undicates that the exons and/or cell types and the exons in a single exon for microarrays having a probe with the exon, where a common pattern of the exons should be assigned to a single exon for gene that the exons should be assigned to a single exon for gene types indicates that the exons should be assigned to a single exon for gene, patricularly expression analysis, and for identifying exons in a gene, patricularly early separate that the exons should be assigned to a single exon for gene, patricularly early separate that the exons should be assigned to a single exon for gene, patricularly early separate that the exons should be assigned to a single exon for gene, patricularly early separate that the exons should be assigned to a single exon for gene, patricularly early separate that the exons should be assigned to a single exon for the study of lung diseases

(CCPD), interestive family context, chronic obstructive pulmonary diseases

(CCPD), interestive family context, chronic obstructive pulmonary diseases

(CCPD), interestive family conte
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Best Local S
Matches 22
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                                                                                                                                                                  Serpentine transmembrane antigen of the prostate; STRAP-1; prostate; transmembrane domain; type Illa membrane protein; expression; cancer; prostate cancer; bladder cancer; colon cancer; parcetate cancer; bladder cancer; colon cancer; parcetate cancer; blander cancer; colon cancer; parcetate; tumour antigen; immuna response; celular; humoral; anticancer vaccine; antibody; detection; diagnosis; celular; humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis; monitoring; susceptibility; therapeutic inhibitor;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the printed specification, but was format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59
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                                                                       sapiens
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         Location/Qualifiers
                                                                                                                                               recombinant
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100.0%; Pred. No. 3.8e-11;
tive 0; Mismatches 0;
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RAITANO A B.
SAFFRAN D C.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate cDNA encoded protein #72.
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                                                                                                                       Claim
                                                                                                                                                                               New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                            WPI; 2001-639232/73.
N-PSDB; AAS64160.
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10-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                              Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORIXA CORP.
                                                                                                                       Page 549; 579pp;
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Pred. No. 1.4e-10;
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Carter D;
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Tang Zhao

Yang Liu C, Wang D,

Drmanac RT, Asundi V, Wang J, Zhang J, Ren Wejhrman T, Goodrich R;

zhou Chen

쯧잗 u C, Wang Cao Y, ang ZW;

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2001-476283/51. DB; AAK51978.

(HYSE-) HYSEQ INC.

03-FEB-2000; 2000US-0496514 27-ARR-2000; 2000US-0560875, 20-JUN-2000; 2000US-05980775, 19-JUL-2000; 2000US-0523325, 01-SEB-2000; 2000US-054936, 15-SEB-2000; 2000US-054936, 15-SEB-2000; 2000US-054936, 10-NOV-2000; 2000US-053325

The invention relates to isolated prostate-specific polymuleotides, polymeptides, service in service in the polymeptides, antibodies raised against the polymeptides (or antigenic epitopes

The invention relate so polynucleotides (ANXS1456-ANXS343) and the encoded polypeptides (ANYS321-ANMS302) that exhibit activity elating trytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or polynucleotides and polypeptides are useful in gene therapy.

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Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -

Claim

Page 3800-3801; 6221pp; English.

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RESULT 8
AAM78845
ID AAM
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         derived from them) and antigen-presenting cells expressing the presence of polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polymocleotides and the antigen-presenting cells are useful for attumbating and/or expanding T cells specific for a tumbus procein, and for inhibiting the development of cancer especially prostate concer. Compositions comprising the polymocleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The obsquare belief is useful for etecting cancer, The present sequence is a prostate specific
                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
05-FEB-2001; 2001WO-US04098
                                                                                                WO200157190-A2
                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                              Human protein SEQ ID NO 1507.
                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                              AAM78845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM78845 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide
                                              09-AUG-2001
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                                                                                                                                                                                         system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention.
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                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 339
                                                                                                                                                                                                                                                                                                                                                            entry)
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Pred. No. 1.4e-10;
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Query Match
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Matches 23
The present invention describes polymucleotide sequences (I) which encode prostate-specific protectins (II), (II) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and because to (II), fusion protects comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is disposed or treated is particularly prostate cancer. (I) and (II) can be used for wontioring the progression of cancer in a patient. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve dispositic and therapeutic methods for postate cancer. They can indicate the level of metastasis as well as the prostate volume. AMH93357 to AMH93944 and AMM01115 to AMM01118 represent polymucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalos MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a for use in vaccines -

    g. stem call growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity; immunomodulatory activity and
activin/inhibin activity and may be useful in the diagnosis and/or

                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-425873/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JAN-2000; 2000US-0483672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; prostate-specific; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P789P amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide therapy. The polypeptides have various cytokine-like activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JAN-2001; 2001WO-US01574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Page 510-512; 543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Mitcham MD, Fanger GR, Day
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100.0%; Pred. No. 1.4e-10;
tive 0; Mismatches 0;
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Retter MW, Stolk JA,
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olk JA, Skeiky YAW;
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           The present invention relates to methods of detecting a prostate cancer associated transcript in a cell from a parient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polymicleorides (designated PC genes) that prostate cancer-associated polymicleorides (designated PC genes) that contact the prostate cancer-associated polymicleoride sequences to them. The prostate cancer-associated polymicleoride sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various or prostate cancer and are derived from the tissues of various and one of the invention are useful for diagnosing and treating prostate cancer. The machods or treating prostate cancer-associated genes are useful for diagnosing or treating prostate cancers, as well as for useful for diagnosing or treating prostate cancer that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as vaccine or in antisense applications.

20 ABG61800-ABG61944 represent prostate cancer-associated proteins.
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Matches 23
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                                                                                                                                                                                                                                                                                                                    Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer associated gare expressed in a prostate tissue
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-471335/50.
N-PSDB; ABK92128.
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                                                                                                                                                                                                                                                                                         Claim 27; Page 312; 436pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2001;
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22; Conservative
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2000US-0733288
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Pred. No. 1.4e-10;
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Best Local :
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Matches 22; Conserv
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27-MAR-2000;
09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
29-AUG-2000;
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23-SEP-1998;
15-JAN-1999;
09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
                                                                                                                      (XUJJ/)
(DILL/)
(MITC/)
(HARL/)
(JIAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
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                           (FANG/)
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01-AUG-1997;
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                                                                                                              (KALO/)
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LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
                                                               DILLON D C.
MITCHAM J L.
MITCHAM J L.
HARLOCKER S L.
JIANG Y.
KALOS M D.
FANCER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                         2000US-0483672.
2000US-0536857.
2000US-0568100.
2000US-0570737.
2000US-053793.
2000US-063793.
2000US-0635215.
2000US-0635215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 116; DB 23; ilarity 100.0%; Pred. No. 1.4e-10; Conservative 0; Mismatches 0;
                                                                                                                                                                                                 2000US-0657279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                2000US-0679426
2000US-0685166
                                                                                                                                                                                                                                                                                   99US-0232149.
99US-0288946.
99US-0352616.
99US-0439313.
99US-0443686.
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                                                                                                                                                                                                                                                                                                                                                      98US-0020956.
98US-0030607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local S
Matches 22
                                                                       Tang YT, Liu C,
Zhao QA, Wang D,
Xue AJ, Yang Y,
                                                                                                                                          03-FEB-2000;
27-APR-2000;
20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a protein described in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New prostate-specific polynuclectides for diagnosing and treating disease, in particular prostate cancer, and as markers for the progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y,
Panger GR, Retter MM, Stolk JA, Day CH, Vedvick TS,
Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoissis; tissue growth factor; namunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 879; 87pp; English
                 Nucleic acids encoding polypeptides with cytokine-like activities useful in diagnosis and gene therapy -
                                              WPI; 2001-476283/51.
N-PSDB; AAK52962.
                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                             Human protein SEQ ID NO 3475.
                                                                                                                                                                                                                                                                                                                                                               06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                   AAM79829;
                                                                                                                                                                                                                                                                                                                                                                                                    AAM79829 standard; Protein; 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-255649/30.
Claim 20; Page 350; 6221pp; English
                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                  30-NOV-2000;
                                                                                                                                                                                                                    05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                         09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 AA;
                                                                                                                                 2000US-0560875
2000US-0598075
2000US-0620325
2000US-0654936
2000US-0654936
2000US-0663251
2000US-0693325
2000US-0728422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                   2000US-0496914
                                                                        Drmanac RT, Asundi V,
Wang J, Zhang J, Re
Wejhrman T, Goodrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                       Asundi V, conq J, Ren F,
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Pred. No. 1.4e-10;
Mismatches 0;
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F, C
                                                                                    Chen
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Wang
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Carter D;
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Ma × ç Gaps

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RESULT 13
AAE02780
ID AAE02
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গ
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to polynuclectides (AMKS1456-AMKS345) and the encoded polypeptides (AMMS323-AMMS302) that exhibit strivity elating to cycokine, cell proliferation or cell differentiation or which may induce production of other cycokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hemanopodesis regulating e.g. stem cell growth factor activity, hemanopodesis regulating activity issue growth factor activity, hemanopodesis regulating activity tand may be useful in the diagnosis and/or restment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
WO200140276-A2
                                                                                                                                                      Domain
                                                                                                                                                                                    Domain
                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cytostatis; antiproliferative; vaccine; gene therapy;
six transmembrane epithelial antigen of the prostate-1, GTEAP-1,
chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human six transmembrane epithelial antigen of prostate (STEAP)-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE02780;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE02780 standard; Protein; 375 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                         Misc-difference
                                                                                                                           Region
                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 REVIHPLATSHOOYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVIHPLATSHOOYFYKIPILV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       /label= Immunogenic_peptide #1
                                                                                   label
                                                                                                                                                                  label= Transmembrane_domain #4
                                                                                                                                                                                                label= HLA-A2_binding_peptide #1
                                                                                                                                                                                                                  65..173
                                                                                                                                                                                                                                                          label= HLA-A2_binding_peptide #5
                                                                                                                                                                                                                                                                                  label= Transmembrane_domain #2
                                                                                                                                                                                                                                                                                                               label= HLA-A2_binding_peptide #2
                                                                                                                                                                                                                                                                                                                                         label= Transmembrane_domain #1
                                                       label
                                                                                                             abel- HLA-A2_binding_peptide #3
                                                                                                                                     abel= Transmembrane_domain #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                   = HLA-A2_binding_peptide #4
                                                                               = Transmembrane_domain #6
                         "Encoded by TTGTAGAAT"
                                                                                                                                                                                                                            Transmembrane_domain #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 116; DB 22;
Pred. No. 1.5e-10;
Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2111 (AAKS2582) and 3666 from the sequence listing
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The present sequence is human six transmembrane epithelial antigen of Ct the prostate (STEAP)-1 protein of clone 10. STEAP is a member of cell curiace serpentine transmembrane antigens. STEAP-1 gene is located on Ct chromosome 7p22.3 and is used in gene therapy. Inhibiting the development CC on progression of a cancer (eg. prostate, colon, bladder, lung, ovarian CC and pancreatic) expressing STEAP or inhibiting growth or killing cells expressing STEAP, comprises administering a vaccine CC expresses STEAP, or inhibiting growth or xilling cells expressing STEAP, comprises the variable domains of the heavy and composition to the patient. Treating a patient with a concer that CC composition antibody that comprises the variable domains of the heavy and composition to the monoclonal antibody that specifically binds to STEAP, comprises the variable domains of the heavy and complied that the vector delivers the single chain monoclonal antibody coding could be sequenced to the cancer cells and the encoded single chain monoclonal control of the patient of the patie
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cancer -
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N-PSDB; AAD07067.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 1A-1B; 187pp; English
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375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hubert RS,
ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epithelial antigen of the prostate) cancers, useful for detecting and t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitchell
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Matches
                                                         Query Match
                                                 Local
                1 REVIHPLATSHQQYFYKIPILV 22
REVIHPLATSHOOYFYKIPILV 113
                                                 Similarity
                                       Conservative
                                                 100.0%;
                                       o,
                                                 Score 116; DB 22;
Pred. No. 1.5e-10;
                                        Mismatches
                                                          Length
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AAY11840 standard; Protein; 95

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AAY11840

18-JUN-1999 (first entry)

Human ų secreted protein SEQ ID No: 440

Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy, chromosome mapping; signal peptide; prostate; upptream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematoppiesis regulation; tissue growth regulation; reproductive hormone; regulation; chamotactic; chamokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.

WO9906550-A2 Homo sapiens

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RESULT 15
AAY12304
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Best Local
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                                                                                                                                                                                                         Human; secreted protein; EST; expressed sequence tag; diagnosis; foresaic; gene therapy, chromosome mapping; signal psptide; upstream regulatory sequence; cytokine activity; cell proliferation; upstream into homomic psptiation; tissue growth regulation; reproductive hormonic regulation; chemotactic; chemothetic, haemostatic; reproductive hormonic regulation; chemotactic; chemothetic, chemothetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity, tissue growth regulating activity, reproductive hormone regulating activity, heamostatic oftended activity, heamostatic and thrombolyvic activity, receptor/ligand activity, anti-inflammatory, activity, the most activity and activity and activity of the sequences. The products can be used in forensic gene therapy and chromosome mapping procedures. The sequences of also be used for obtaining corresponding promoter sequences of the mucleic acids encoding the signal peptides can be used for differential section of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human secreted proteins expressed in prostate, and encode the proteins given in ANY11716 to ANY11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene nucleic acid sequences can be used for producing secreted human gene
                 01-AUG-1997;
                                                                                                                                                                                                                                                                                                                    Human 5' EST secreted protein SEQ ID NO:335.
                                                                                                                                                                                                                                                                                                                                                          17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY12304 standard; Protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cyrokine activity, cell proliferation and differentiation activity. Haematopoissis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 34; Page 577; 675pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1997;
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                                                 31-JUL-1998;
                                                                                                                       WO9906548-A2
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                          thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 REVIHPLATSHOOYFYKI 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-153780/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                          anti-inflammatory; tumour inhibition
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                 97US-0905135
                                                 98WO-IB01222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83.6%;
100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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1 REVIHPLATSHQQYFYKI 18 REVXHPLATSHOOYFYKI 109

Matches Query Match

Local

Similarity

Score 92; DB Pred. No. 3.1e 0; Mismatches

3.1e-07; DB 20;

Length 109 Indels

0 Gaps

0

Conservative 79.3%; 0

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CC human secreted protesins, and encode the protesins given in AAV1251 to CC having the respectively. The protesins given represent the signal peptide and an N-terminal fragment of a secreted human gene products. They come also be used to develop producing secreted human gene products. They can also be used to develop producing secreted human gene products. They come in the protesins obtained may have cyrokine activity, call and therapy. The composition of the protesins of the products for disapposis and therapy. The composition of the protesing activity, the products of the products of the products of the products of the products of the products of the products of the products of the products of the products of the products of the products of the sequences can also be used for obtaining corresponding promoters can be used in foreign encoding the signal peptide on be used for discriming extracellular secretion of a polypeptide or the insertion of a polypeptide or the products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding human secreted proteins - obtained from CDNA libraries prepared from e.g. liver, ovary, brain, prostate, kidney, lung, umbilical cord, placenta and colon tissue
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; Page 677; 824pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-153778/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX41094 to AAX41347 represent 5' expressed sequence tags
                                               polypeptide into a membrane, or importing a polypeptide into a cell.
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109 AA;
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Run

9

OM protein -

protein search, using sw

model

Copyright

GenCore version 5.1.4\_p5\_4578 (c) 1993 - 2003 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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98603 arabidopsis
Q10638 mycobacteri
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Q29109 mas museulu
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99UEB; 0955034; 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
15-UUN-2002 (Rel. 41, Last annotation update)
Six transmembrane epithelial antigen of prostate.
                            TRANSMEM
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EMBL; AC005053; AAC79150.1;
EMBL; AC004969; AAD15620.1;
EMBL; BC011802; AAH11802.1;
Genew; HGNC:11378; STEAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human prostate tumors.";
Proc. Natl. Acad. Sci. U.S.A. 96:14523-14528(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEDILNE-2005627; PubMed=10589738;
Hubert R.S. Vivanco I., Chen E., Rastegar S., Leong K.,
Mitchell S.C., Madraswala R., Zhou Y., Kuo J., Raitano A.B.,
Jakobovite A., Saffran D.C., Afar D.B. H.;
"STEAP: a prostate-specific cell-surface antigen highly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Abu-Threideh J., Stoneking T., Langston Y., Maupin R.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STEAP OR STEAP1.
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PLC LISMO
MNN9 YEAST
C11A RAT
PARC BORBU
HRPI PSESY
VGLB VZVD
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       55443A170C870387 CRC64;
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4 listeria mo
7 saccharomyc
7 rattus norv
6 borrelia bu
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7 varicella-z
7 xylella fas
5 herpes simp
1 herpes simp
7 herpes simp
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Result No.

Score

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100.0 Match Query

STEA\_HUMAN CIXG\_HAEIN MSRA\_HALN1 CYF\_PORPU

47.5

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YD27 MYCTU CYAA SACKL SYFA ARATE

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FRAP MOUSE
SPAI FIG
FYRE METAC
RPBS DROME
RPKI TEAST
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VALE HSVBC
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Database

SwissProt\_40:\*

Listing first 45 summaries

Post-processing: Minimum Match 0% Maximum Match 100%

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length: 0 length: 2000000000

Total number

hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Scoring table: Sequence: Title: Perfect score:

Gapop 10.0 , BLOSUM62

Gapext

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US-10-010-667A-19 116

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RESULT
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PlateChmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.P. RelateChmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M. McKenney K., Butt C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kalley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kalley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D., Weldman J.F., Hanna W.C., Mgyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fahrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
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15-JUN-2002 (Rel. 41, Last sangustion update)
15-JUN-2002 (Rel. 41, Last sangustion update)
16-XUN-2002 (Rel. 41, Last sangustion update)
16-XUN-2004 (Rel. 41, Last sangustion update)
16-XUN-2004 (Rel. 41, Last sangustion update)
16-XUN-2004 (Rel. 41, Last sangustion update)
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16-XUN-2004 (Rel. 41, Last sangustion update)
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                                    SEQUENCE
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Science 269:496-512(1995)
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                                                                                                                                                                                                                             Complete
                                                                                                                                                                                                                                                            Transferase; Nucleotidyltransferase; Lyase; Multifunctional enzyme;
                                                                                                                                                                                                                                                                                                Pfam; PF01874; CitG;
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                                                                                                                                                                                                                                                                                                                                         nterPro; IPR002736;
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TRIPHOSEMORIDOSYL) -1'-DEPHOSEMOCHONZYME-A, AND THEN THE TRANSFER
OF THIS PROSTHETIC GEOUP RECURSOR TO THE APO-ACYL CARRIER PROTEIN
(GAWAN, CHANI) OF THE CITRATE LYASE TO YIELD THE HOLO-ACYL CARRIER
RROTEIN (BY SIMILARITY)
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                                                                  APO-CITRATE LYASE PHOSPHORIBOSYL-
DEPHOSPHO-COA TRANSFERASE.
2-(5''-TRIPHOSPHORIBOSYL)-3'-
DEPHOSPHOCOENZYME-A SYNTHASE.
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Pred. No. 2.5e-11;
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Dougherty B.A., Merrick J.M.,
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
methionine-Soxide reductase) (Feptide Met(O) reductase)
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                                                                                                                                                                     EMBL; AE005045; AAG19555.1; ... HSSP; P54149; 1FVA.
                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Halobacteriaceae; Halobacterium.
                                                              SEQUENCE
                                                                                                         TIGRFAMS; TIGRO0401; msrA;
                                                                                                                          ProDom; PD003489; PMSR; 1.
                                                                                                                                       Pfam; PF01625; PMSR; 1.
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Similarity
9; Conser
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  Conservative
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50.0%;
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Pred.
            Score 49; DB 1
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  Mismatches
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                              DB 1;
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                                       SYFA ARATH STAN
Q9T034;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                       CHAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISG-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatice Institute of Bioinformatics are no restrictions on its the Buropean Bioinformaticutions as long as its content is also no way modified and this stagement is not removed to be a supported by and for commercial contents.
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P51265;
          16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Probable phenylalamyl-trRNA synthetase alpha chain
(Phenylalamine--RNA ligase alpha chain) (Phens).
                                                                                                                 ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002325; Apocyt_F.
InterPro; IPR00235; CytC_heme_bind.
Pfam; PF0133; Apocytochrome_F; 1.
PR1NTS; PR00610; CTTOCHROMEF;
PROSITE; PS00190; CTTOCHROME_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U38804; AAC08151.1; -. HSSP; P36438; 1HCZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome.";
Plant Mol. Biol. Rep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Avonport;
Reith M.E., Munh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Rhodophyta;
NCBI_TaxID=2787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apocytochrome
PETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last
16-OCT-2001 (Rel. 40, Last
                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                 Photosynthesis; Photosystem I; Photosystem II; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence of the Porphyra purpurea chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porphyra purpurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                     TTGHEMETOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
AT4G39280 OR T22F8.180
                                                                                                                                                                            160
                                                                                                                                                                                                       1 REVIHEL----ATSHOOYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MEMBER OF THE CYTOCHROME B6/F COMPLEX INCLUDING CYTOCHROME B6, CYTOCHROME F AND PROBABLY AN IRON SULFUR PROTEIN. SUBCELULUAR LOCATION. Chloroplate thylakoid membrane (Probable). SIMILARITY: BELONGS TO THE CYTOCHROME C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: TRANSLOCATES PROTONS ACROSS THE THYLAROID MEMBRANE AND TRANSFERS ELECTRONS FROM PHOTOSYSTEM II TO PHOTOSYSTEM I. IT RECEIVES ELECTRONS FROM THE ALBEKE IRON-SULFUR PROTEIN AND PASSE THEM TO PLASTOCYANIN; THIS FUNCTION IS VERY SIMILAR TO THAT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRIAL CYTOCHROME C1.
                                                                                                                                                                            REIIFPILSPDPAKDKQAHFFKYPIYV 186
                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               transport; Heme; Chloroplast; Thylakoid;
                                                                                                                                                                                                                                                                                              320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Munholland J.;
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                             57
57
60
61
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                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                              35012 MW;
                                                                                                                                                                                                                                                  40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bangiophyceae; Bangiales; Bangiaceae; Porphyra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                  Score 47.5,
Pred. No. 2
                                                                                                                                                                                                                                                                                                                        APOCYTOCHROME F.
HEME (COVALENT) (PROBABLI
HEME (COVALENT) (PROBABLI
IRON (HEME AXIAL LIGAND)
                                                                                                                                                                                                                                                                                                                                                                                    CHLOROPLAST (BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                    PRT;
                                                                                                                                                                                                                                                                                              C9B103F0453369C7 CRC64,
                                                                                                                                                                                                                                      Mismatches
                                                                                                    474
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                                                                                                                                                                                                                                                    В,
                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                                                           (PROBABLE).
                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                 Length 320;
                          (EC 6.1.1.20)
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THAT OF
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ANALYMETER, N., Schneller C., Manbutt R., Murphy G., Volckaert G., RA Mayer K. T., Duesterhoeft A., Stickema W., Entlan K.-D., Terryn N., RA Harris B., Anasorge W., Brandt P., Grivell L.A., Reger M., Meller M., Rachiselgariner M., de Simone V., Obermaier B., Mache, Meller M., Reichselgariner M., de Simone V., Obermaier B., Mache M., Meller M., Reichselgariner M., de Simone V., Obermaier B., Mache M., Meller M., Reichselgariner M., Delaeny M., Diddomencch P., Watson M., Schmidtheill T., Rakelchert B., Porietelle D., Perez-Alonso M., Boutty M., Bancroft I., Rakels M., Weltysheld M., Delaeny M., Delaeny M., Delaeny M., Bancroft I., Rakels M., Schmidtheil T., Rakels M., Schmidtheil T., Rakels M., Rakels M., Schmidtheil T., Rakels M., Schmidtheil T., Rakels M., Rakels M., Schmidtheil T., Rakels M., Rakels M., Schmidtheil T., Rakels M., Rakels M., Rakels M., Lambarth S., Van den Daele H., Rakels M., Rakels M., Lambarth S., Van den Daele H., Rakels M., Rakels M., Lambarth S., Van den Daele H., Rakels M., Rakels M., Lambarth S., Van den Daele H., Rakels M., Rakels M., Lambarth S., Van den Daele H., Rakels M., Rakels M., Lambarth S., Van den Daele H., Rakels M., Lambarth S., Wayes R., Rettett A., Rajandream M.A., Lyne M., Benes V., Rechman S., Rakels M., Lambarth S., Dauner D., Herzl A., Rakels M., Lambarth S., Dauner D., Herzl A., Rakels M., Lambarth S., Dauner D., Herzl A., Rakels M., Lambarth M., Lambarth S., Dauner D., Herzl A., Rakels M., Lacherry A., Ambourg S., Rakels M., Marisa D., Bent B., Mohnson S., Tacon D., Torres A., Berger C., Wonfort A., Cacacherta E., Bergel L., Rakels M., Marisa M., Marisa M., Marisa M., Marisa M., Marisa M., Authers S., Geisel C., Lawan D., Rakels M., Bent B., Marisa M., Authers S., Geisel C., Lawan D., Rakels M., Maris
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceee, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 402:769-777(1999).

-I- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) =
-I- diphosphate + L-phenylalanyl-tRNA(Phe).
-I- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS (BY
                                                                                                                                                                                                                  This SMISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatitle European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20083488; PubMed=10617198;
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                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Cytoplaemic (By similarity).
SIMILARITY: BELONGS TO CLASS-II AMIDOACYL-TRNA SYNTHETASE FAMILY.
PHE-TRNA SYNTHETASE ALPHA CHAIN SUBPAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
AL161594; CAB80591.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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Best Local S
Matches
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YD27_MYCTU
Q10638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SESQUENCE FROM N.A., White O., STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Fleischmann R.D., Alland B., Skinn M.L., Hatt D., Hickey E., Peterson J., DeBoy R., Dodson R., Oshinn M.L., Brobleva M.D., Salzbergi Kolonay J.F., Welson M.C., Umyawa L.A., Ermoleeva M.D., Salzbergi Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula Jelcher A., Weidman J., Khouri H., Gill J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman J., Weidman
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
Gordon S.V., Eiglmeter K., Gas S., Barry C.E. III, Tekaia F.,
Gordon S.V., Eiglmeter K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Comnor R.,
Davtes R., Devlin K., Feltwell T., Gentles S., Hanlin N., Holroyd S.,
Davtes R., Devlin K., Krogh A., McLean J., Moule S., Murphy L.,
Oliver S., Osborne J., Quali M.A., Rajandream M.A., Rogers J.,
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulaton J.E., Taylor K., Whitehead S., Barrell B.G.,
Sulaton J.E., Taylor K., Whitehead S., Barrell B.G.,
Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
-01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Hypothetical protein RV1327C.
RV1127C OR MT156 OR MTCY130.12C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEdam; PRO1409; tRNA-synt 2d; 1.
TICREPMs; TIGRO468; pheS; 1.
PROSITE: PS50862; AA_TRNA_LICASE II; 1.
Aminoscyl-tRNA synthetase; Protein blosynthesis; Ligase; ATP-binding
SEQUENCE 474 AA; 54516 MM; OPETF1BA07C03C77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                        Tuberculist, Rv1327c; -.
InterPro; IPR000461; Alpha_amylase.
                                                                                                                          EMBL; AE007010
TIGR; MT1369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                  EMBL; 273902; CAA98091.1; -.
                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Whole genome comparison of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                         AE007010; AAK45633.1;
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR004529; Phes.
IPR002319; tRNA-synt_2d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR002106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.7%;
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Pred. No. 7
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SMART;
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01-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=91323718;
MEDLINE=91323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces kluyveri (Yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adenylate
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InterPro; IPR001611; LRR.
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mes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IS SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation the Swiss Institute of Bioinformatics and the EMBL outstation on the Employer of the Collaboration of the Employer
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SIMILARITY: BELONGS TO ADENYLIL CYCLASE CLASS-3 FAMILY.
SIMILARITY: CONTAINS 21 LEUCINE.RICH REPEATS (LRR).
SIMILARITY: CONTAINS 1 PP2C-LIKE DOMAIN.
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JQ1145; JQ1145
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Last annotation update)
(4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
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Pred. No.
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                                                                                                                                                                                                                        synthesis; Magnesium
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FRAP_MOUSE
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Best Local
MGD: MGI 192894, Frap.,
InterPro; IRR03151; FAT.
InterPro; IRR03151; FAT.
InterPro; IRR03152; FATC.
InterPro; IRR03152; FATC.
InterPro; IRR000457; HAT repeat.
Pfam; PF00454; PI3 PI4 kinase; 1.
Pfam; PF00259; FATC; 1.
SMART; SM00146; PIXE; 1.
SMART; SM00146; PIXE; 1.
                                                                                                                                                                     FRAP MOUSE
Q9JLN9;
16-OCT-2001
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                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seguence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                  EMBL; AF152838; AAF73196.1; -. HSSP; P42345; 1FAP.
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 46; DB 1; Length 1839;
Pred. No. 35;
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Best Local Similarity
Matches 8; Conserv
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028930, (8el. 40, Created)

16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 40, Last amoration update)

16-0CT-2001 (Rel. 40, Last amoration update)
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PROSITE;
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SMART; SM00042; CUB; 1.

PROSITE; PRO096; SPERMADHESIN 1; 1.

PROSITE; PRO196; SPERMADHESIN 2; FALSE_NEG.

PROSITE; PRO1180; CUB; 1.

PROSITE; PRO1180; Glycoprotein; Fertilization; Signal.

SIGNAL 21 SEMINAL PLASMA SPERM MOT

CHAIN 12 SEMINAL PLASMA SPERM MOT
                                                                                                                                                                                                                                                                                                                                                    the Buropean Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ogada T., Gagnon C.;
"Cloning of boar SPMI gene which is expressed specifically in seminal vesticle and codes for a sperm mortility inhibitor protein.";
FEBS Lett. 38420-4441995).
-i- FUNCTION: INNIETTOR OF SEBEM MOTILITY.
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                                                                                                                                                              InterPro; IPR000859; CUB_domain.
InterPro; IPR000124; Spermadhesin
Pfam; PF00431; CUB; 1.
                                                                                                                                                                                                                                       EMBL; S80568; AAB35000.2; -. HSSP; P29392; 1SFP.
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
-!- SIMILARITY: BELONGS TO THE SPERMADHESIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUB SPECIFICITY: SEMINAL PLASMA OR SPERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iwamoto T., Hiroaki H., Furuichi Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE=Seminal vesicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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PS50077;
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PI3_4_KINASE_3; 1.
HEAT_REPEAT; FALSE_NEG.
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HEAT 2.
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HEAT 5.
HEAT 6.
HEAT 7.
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   BY SIMILARITY.
SEMINAL PLASMA SPERM MOTILITY INHIBITOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wada K.,
                                                                                                                                                                                                                                                                                                                                    noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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RA FiltHugh W., Calvo S., Engels R., Smirnov S., Annoor D., Brown A.,
RA Hilen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Lincon L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Limbor A., Darber R.D., Cann I., Graham D.E., Grahame D.A.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Muhopadhyy B., Reve V.J.N., Smith K.,
RA Springer T.A., Umayam L.A., Mhite O., White R.H., de Meario B.C.,
RA Springer T.A., Umayam L.A., Mhite O., White R.H., de Meario B.C.,
RA PFILChett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.,
RA Metcalf W.W., Birren B.,
RY "The genome of Methanosarcina acetivorans reveals extensive metabolic
r and physiological diversity.",
L Genome Res. 12:532-542(2021)
C. - CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
                                                           Query Match
Best Local S
Matches 12
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                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMPL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q8THL2;
                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last nanotation updat)
Aspartate carbamoyitransferase (EC 2.1.3.2)
                                                                                                                        PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
PYYIMIdine biosynchesis; Transferase; Complete proteome SEQUENCE 308 AA; 34644 MW; 33282B438E28595C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C2A / ATCC 35395 / DSM 2834;
MEDLINE=21929760; PubMed=11932238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
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PYRB OR MA4502.
                                                                                                                                                                         EMBL; AE011170; AAM07842.1;
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262
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                              2 EVIHPL-----ATSH----QQYFYKIPI 20
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KVLHPLPRVNEIAPEVDATPHACYFEQAFYGVPI 295
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                                                           Score 44.5; DE
Pred. No. 8.1;
4; Mismatches
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BY SIMILA
N-LINKED
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Pred. No. 3.
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9DC107799A4C71EF CRC64;
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2.1.3.2) (
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RESULT 11
RPB2_DROME
            Adams M. R. Celniker S.E. H. D. W., Hoskins R.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Lib P.W., Hoskins R.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Richards S. Ashburner M., Henderson S.N.,
R. Amanacides P.G., Scherer S.E., Lib P.W., Hoskins R.A., Galle R.E.,
R.A. Amanacides P.G., Scherer S.E., Richards S. Ashburner M., Henderson S.N.,
R. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Champ
R. Ashburner M. C., Rogers Y.-H.C., Blazej R.G., Champe M., Freifier B.D.,
R.A. Man K.H., Doyle C., Baxder E.G., Helt G., Welson C.R., Miklos G.L.G.,
R.A. Man K.H., Doyle C., Baxder E.G., Helt G., Welson C.R., Miklos G.L.G.,
R.A. Man K.H., Doyle C., Baxder E.G., Helt G., Welson C.R., Miklos G.L.G.,
R.A. Maril J.F., Agbayani A., An H.-J., Andrews-Plannsch C.C., Baddwin D.,
R.A. Basu A., Base A., Baxena B.P., Bandari D., Bolshakov S.,
R.A. Backova D., Botcham M.R., Bouck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottier P.,
R.A. Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottier P.,
R.A. Dodgen K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dodgen K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dodgen K., Doup L.E., Correll J.H., G. Z., Guan P., Harris M.,
R.A. Dodgen K., Doup L.E., Correll J.H., G. Z., Guan P., Harris M.,
R.A. Fooler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
R.A. Glodek A., Cong F., Gorrell J.H., Gu Z., Guan P., Harris M.R.,
R.A. Fooler C., Garrill J.H., Gu Z., Guan P., Harris M.R.,
R.A. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R.A. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R.A. Harris N.L., Martel B., McIntosh T.C., McLed J., Wei M.-H., Degvam C.,
R.A. Harris N.L., Martel B., McIntosh T.C., McLed M.P., Kall D., Lai S.,
R.A. Harris N., McMartel 
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01-NUG-1988 (Rel. 08, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase II 140 kba polypeptide (EC 2.7.7.6)
(RNA polymerase II subunit 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palkenburg D., Dworniczak B., Faust D.M., Bautz E.K.F.;
"RNA polymerase II of Drosophila. Relation of its 140,000
to the beta subunit of Escherichia coli RNA polymerase.";
J. Mol. Biol. 195:929-937(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila mėlanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda, Mandibulata, Pancrustacea; Hexapoda;
Insecta; Pterypota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 100:155-162(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sitzler S., Oldenburg I., Peterson G., Bautz E.K.F.;
"Analysis of the promoter region of the housekeeping gene DmRP140 by
sequence_comparison of Drosophila melanogaster and Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPII140 OR CG3180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91276237; PubMed=1905256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissum=Embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-69 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=88011299; PubMed=3116266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 54-1176 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DROME
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFXL YEAST
P48743;
01-FEB-1996
15-JUL-1998
15-JUN-2002
         STRAIN-SCREO / AB972,
MEDLINE-9731267; PLAMED-1869871;
MEDLINE-9731267; PLAMED-1869871;
Johnston M., Hiller L., Riles L., Albermann K., Andre B., Ansonence V., Bruckner M., Delius H., Dubois E., Dusterhoft A.,
Entlan K.D., Floeth M., Goffeau A., Hebling U., Heumann K.,
Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P.,
Louis E.J., Messenguy F., Mawes H.-W., Missea T., Mostl D.,
Louis E.J., Messenguy F., Mawes H.-W., Missea T., Mostl D.,
Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISG-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wall modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to licenseeibb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical 90.6 kD
YLR176C OR L9470.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; DNA-directed RNA polymerase; Transcription; Zinc-finger, Metal-binding; Nuclear protein.
ZN_FING 1121 1142 C4-TYPE [POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0003276; RpII140.
InterPro, IPR001572; RNA pol B.
Pfam; PF00562; RNA pol B; 1.
PR051TE; P501166; RNA FOL BETA; 1.
Transferase; DNA-directed RNA poly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X05709; CAA29180.2; -.
EMBL; M62972; AAA288476.1; -.
EMBL; AE003703; AAAE55024.1; -.
PIR; A27826; A27826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
-I- FUNCTION: DNA-DEPRIDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 EGLDPVETQHQKTFIGKIPIML 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYMERASE II.
SUBCELLULAR LOCATION: NUCLEAT INC-CONTAINING RANMISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RANFOLL BOLLD IN BUSANCOTIC NUCLEI: POLYMERASE I FOR THE PRECURSOR, POLYMERASE II FOR THE MENA PRECURSOR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: EACH CLASS OF RNA POLYMERASE IS ASSEMBLED FROM 9 TO 14 DIFFERENT BOLVEPETIES. RNA POLYMERASE II CONSISTS OF 10 DIFFERENT SUBUNITS. THIS SUBUNIT IS THE SECOND LARGEST COMPONENT OF RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: N nucleoside triphosphate = N
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                                                                                                                                                                                                                                                                                                                                                             TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 (Rel. 33, Created)
8 (Rel. 36, Last sequ
12 (Rel. 41, Last anno
aal 90.6 kDa protein i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
protein in CBF5-DKA1 intergenic region
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Pred. No.
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ID -> MY (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.5;
No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      811 AA.
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E., Pohl T.M.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OUT-2001 (Rel. 40, Last sententian update)
Glycoprotein I precursor (Glycoprotein GVP-6)
Glycoprotein 16) (Glycoprotein GJ30).
                      Glycoprotein; Transmembrane;
SIGNAL 1 67
CHAIN 68 928
                                                                                                                                                                                                                                                                                                                    This SATSS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenses@sib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misra V., Neison R., Smith M.;
Misra V., Neison R., Smith M.;
"Sequence of a bovine herpesvirus type-1 glycoprotein gene
"Sequence of a bovine hernes simplex gene for the glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      homologous to the herpes simplex gene for the glycopro
Virology 166:542-549(1988).
-i- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses,
Alphaherpesvirinae; Vari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                 Pfam, PF00606; Glycoprotein_B; 1.
ProDom; PD000693; Glycoprot_B; 1.
                                                                                                                                                                                                                                                         EMBL; M23257; AAA46013.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE HERPESVIRUSES GLYCOPROTEIN B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=89020821; PubMed=2845660;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine herpesvirus type 1 (strain P8-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          496
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                                                                                                                                                                                                                              A31166 - VGBEBG.
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9; Conserv
                                                                                                                                                                                     IPR000234, Glycoprot_B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        811 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ses, no RNA stage; Herpesviridae;
Varicellovirus.
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GVP-6)

(Glycoprotein 11A)

gB. ";

Signal. GLYCOPROTEIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dortetelle D., Purmelle B., Rechmann S., Rieger M., Rinke M., Rose M., Schaffe M. Scherens B., Schalter P., Schager C., Schwarz S., Vinderwood A.P., Urrestarani I.A., Vandenbol H., Verhasself B., Voet M., Volkaert G., Voss H., Wamburt R., Wedler E., Wedler H., Zimmermann F.K., Zollher A., Hani J., Hohelsel J.D.; "The mucleotide sequence of Saccharomyces cerevisiae chromosome XII.", Nature 387:87-90 (1997).
                                                                                                                                                                            InterPro; IPR003150; RFX DNA binding. Pfam; PF02257; RFX DNA binding; 1. Hypothetical protein.
                                                                                                                                                                                                                                       EMBL; U17246; AAB67470.1; -. SGD; S0004166; YLR176C.

    -!- SIMILARITY: BELONGS TO THE RFX FAMILY.

                                                                           Conservative
                                                                                                                                                         90583 MW; 116A88B7DDE4FBF0 CRC64;
510
                                    19
                                                                                              37.9%;
                                                                           2:
                                                                                              Score 44;
Pred. No.
                                                                              Mismatches
                                                                                                                  DB 1; Length 811;
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101.0CT.189 (Rel. 12 Created)
11.0CT.189 (Rel. 12 Last sequence update)
16.0CT.289 (Rel. 40 Last sequence update)
16.0CT.280 (Rel. 40 Last sequence update)
Clycoprotein I precursor (Clycoprotein OVP-6) (Clycoprotein 1A)
(Clycoprotein 16) (Clycoprotein Glycoprotein B).

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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE-88310884; PubMed=2841484;
MEDILEDECK J.C., EB1D L. J. Lawrence W.C.;
Comparison of the bowline herpesvirus 1 g1 gene and the herpes
simplex virus type 1 g8 gene.";
J. VIRO1. 62:3139-332(1988).
1- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
1- SUBUNIT: DIMER, PROBABLY LINKED BY DISULFIDE BONDS.
                                                                                                                            Glycoprotein; Transmembrane;
SIGNAL 1 67
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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739370;

01-FBB-1995 (Rel. 31, Created)

01-FBB-1995 (Rel. 31, Last seq

16-OCT-2001 (Rel. 40, Last ann
                                                                                        InterPro; IPRO05181; DUP303.

Pfam; PP03629; DUP303; 1.

Rypothetical protein; Signal; Complete proteome.

Rypothetical protein; Signal; Complete proteome.

SIGNAL 22 326 HYPOTHETICAL PROTEIN VIHS

CHAIN 22 326 HYPOTHETICAL PROTEIN VIHS
                                                                                                                                                                                                                                                                                                                      Blattney F.R., Blattney F.R., Stationer VI: DNA sequence "Analysis of the Escherichia coli genome VI: DNA sequence region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                EcoGene; EG12561; yjhS.
InterPro; IPR005181; DUF303.
                                                                                                                                                                         EMBL; U14003; AAA97205.1; -.
EMBL; AE000501; AAC77265.1; -.
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STRAIN=K12 / MG1655;
MEDLINE=95334362; PubMed=7610040;
Burland V.D., Plunkett G. III, Sofia H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia
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10 US-09-747-835A-51
10 US-09-747-835A-51
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10 US-09-875-793-879
10 US-09-885-793-879
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10 US-09-785-143-879
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US-10-010-667A-19
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Sequence 19, Appl
Sequence 10, Appl
Sequence 47234, A
Sequence 50, Appl
Sequence 51, Appl
Sequence 879, App
Sequence 879, App
Sequence 879, App
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Sequence 879, App
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US-10-

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Publication No. US20020045682A1

Publication No. US2002004568A1

APPLICANT: ACAT. Daniel

APPLICANT: ACAT. Daniel

APPLICANT: Habert, Rene S.

APPLICANT: Hebert, Rene S.

APPLICANT: Mitchell. Steve Chappell

TITLE OF INVENION: ANTIBODIES INUNOSPECIFIC FOR STEAPI (AS AMENDED)

FILE REFERENCE: $11952001510

CURRENT FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: US/10/011,095

CURRENT FILING DATE: 1999-06-107

PRIOR APPLICATION NUMBER: 60/07,520

PRIOR APPLICATION NUMBER: 1998-06-01

I PRIOR APPLICATION NUMBER: 1998-06-01

I PRIOR APPLICATION NUMBER: 60/07,520

PRIOR APPLICATION NUMBER: 1998-06-01

I PRIOR APPLICATION NUMBER: 60/07,520

PRIOR APPLICATION NUMBER: 1998-06-01

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PRIOR APPLICATION NUMBER: 1998-06-01

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I PRIOR APPLICATION
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: AGET, Daniel

APPLICANT: AUBELT, Rene S.

APPLICANT: AUBELT, Rene S.

APPLICANT: AUBELT, Rene S.

APPLICANT: BAIGHAN, ARTHUR B.

APPLICANT: SAFFRAN, DOUGLAS C.

APPLICANT: MICHOELL, STOPE CHAPPELL

APPLICANT: MICHOELL, STOPE CHAPPELL

APPLICANT: MICHOELL, STOPE CHAPPELL

APPLICANT: SAFFRANCE: 51582001601

CURRENT PILLING DATE: 2001-12-06

CURRENT PILLING DATE: 2001-12-06

FRIOR APPLICATION NUMBER: 60/007.520

FRIOR APPLICATION NUMBER: 60/007.520

FRIOR PILLING DATE: 1999-06-01

FRIOR PILLING DATE: 1999-06-01

FRIOR PILLING DATE: 1999-06-01

FRIOR FILLING DATE: 1999-06-01

FRIOR PILLING DATE: 1999-06-01

FRIOR FILLING DATE: 1999-06-01

FRIOR FILLING DATE: 1999-06-30

FRIOR FILLING DATE: 1999-06-30
CIMERNY PRILONITION NUMBER: 105/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION WADER: US 60/180,312
PRIOR PLING DATE: 2000-02-04
PRIOR APPLICATION WADER: US 05/610,312
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-05-26
PRIOR PRILING DATE: 2000-10-04
PRIOR PRILING DATE: 2000-10-04
PRIOR PRILING DATE: 2000-05-27
PRIOR PRILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
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SOFTWARE: FASUSEQ for Windows Version
SEQ ID NO 19
LENGTH: 22
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GENERAL INFORMATION:
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APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: AGONICA-K-1
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100.0%; Pred. No. 7.4e-12;
tive 0; Mismatches 0;
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APPLICANT: Ren, fedyen

APPLICANT: ABIN, fedyen

APPLICANT: ABIN, fedyen

APPLICANT: ABIN, fedyen

APPLICANT: Danid, Vinod

APPLICANT: Drandc, Radoje T

ITILE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEDTIDES

TITLE OF INVENTION: LIKE) POLYPEPTIDES AND POLYNUCLEDTIDES

FILE REPERENCE: HTS-7CIP

CURRENT TRING DATE: 2002-03-08

PRIOR APPLICATION NUMBER: US 09/747,835A

CURRENT TRING DATE: 2002-03-08

PRIOR APPLICATION NUMBER: US 09/53,450

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yamazaki, Victoria
APPLICANT: Tang, Y. Tom
                                                                              PRIOR FILING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: US
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                  NUMBER
                                                  PRIOR FILING DATE:
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US20020146692A1

Application US/09747835A

Tang, Y. Tom Liu, Chenghua Zhou, Ping Wang, Dunrui

FILING DATE: 2000-04-25

Q

SEQ ID NOS:

2000-01-21

09/488,725

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US-09-747-835A-50
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NUMBER OF SEQ ID NOS: 49117

NUMBER OF SEQ ID NOS: 49117

SEQ TING 47234

LENGTH: 104
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                               Query Match
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PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PT/US01/00663
PRIOR APPLICATION NUMBER: POT/US01/00662
PRIOR APPLICATION NUMBER: POT/US01/00662
PRIOR APPLICATION NUMBER: POT/US01/00661
PRIOR APPLICATION NUMBER: POT/US01/00661
                                                                                                                                                                                                                                                                                                            OTHER IMPORMATION: EMPRESSED IN LUNG, SIGNAL = 1.5
OTHER IMPORMATION: EXPRESSED IN LUNG, SIGNAL = 0.87
OTHER IMPORMATION: EXPRESSED IN PETAL LUVER, SIGNAL = 0.87
OTHER IMPORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
OTHER IMPORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.59
OTHER IMPORMATION: SISSEPROT HIT OG7305 EVALUE 5.000+00
OTHER IMPORMATION: BST_HUMAN HIT: BE875216.1, EVALUE 7.000-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                               59
                                                                                                                                                                                                                       Local
                                                                                                                              1 REVIHPLATSHQQYFYKIPILV 22
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                                                                                               REVIHPLATSHOOYPYKIPILV 80
                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                   100.0%; Score 116; DB 10; 100.0%; Pred. No. 4.4e-11;
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APPLICANT: Zhang, Jie
APPLICANT: Ren., Reiyan
APPLICANT: Send., Feiyan
APPLICANT: Send., Vined
APPLICANT: Send., Vined
APPLICANT: Drmanac, Radoje T
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: LIKE) POLYPRETIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: LIKE) POLYPRETIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: LIKE) POLYPRETIDES AND POLYNUCLEOTIDES
TILING DATE: 2000-00-08
PRIOR REPLICATION NUMBER: US 09/747,835A
CUBRENT TILING DATE: 2000-00-08
PRIOR APPLICATION NUMBER: US 09/729,739
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/653,450
PRIOR APPLICATION NUMBER: US 09/650,312
PRIOR APPLICATION NUMBER: US 09/550,042
PRIOR PRICATION DATE: 2000-00-02
PRIOR PRICATION NUMBER: US 09/550,042
PRIOR PRICATION 
                                                                                                                                                                                                                          US-10-012-896-879
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US-09-747-835A-51
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                                                                                                                                                   Sequence 879, Appublication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.0
SEQ ID NO 51
LENGTH: 267
                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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Best Local
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ORGANISM: Homo sapiens
-09-747-835A-50
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
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                                                                                                                                                                                                                                                                                                                                              26 REVIHPLATSHOQYFYKIPILV 47
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Wang, Dunrui
                                                                                                                                                       Application US/10012896
o. US20020183251A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020187472A1 g6572948
US-09-802-520-11
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APELICANT: Weacher, Medeleine Joy
TITIE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITIE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
PILE REFERENCE: JANJ21.477C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING BATE: 2001-72-10
NUMBER OF SEQ ID NOS: 1011-72-10
NUMBER OF SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/09802520 Publication No. US20020187472A1
      Matches
                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Vinals de Bassols, Carlota
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Vedvick, Thomas
Carter, Darrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky, Yasır A.W.
Hepler, William T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Henderson, Robert A.
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      Conservative
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ick, Thomas S.
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Pred. No. 1.7e-10;
                                      Score 116; DB 9;
Pred. No. 1.7e-10;
      Mismatches
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1 REVIHPLATSHQQYFYKIPILV 22

REVIHPLATSHOOYFYKIPILV 113

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Sequence 879, Application US/0895793

Pablication No. US20020192763A1

GENERAL INFORMATION

APPLICANT: XI, Jiangchun

APPLICANT: Milcham, Jornifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yuqiu
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TITLE OP INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OP INVENTION: COMPOSITION FOR PROSTATE CANCER FILE REFERENCE: 2101.21.534CCUS.059895,793

CURRENT APPLICATION WOMBER: US/09/895,793

CURRENT PILLING DATE: 2001-06-29

NUMBER OF SEQ ID NOSE: 982

SOPTARE: PastSEQ FOR Windows Version 3.0

SEQ ID NO 892

ENOTH: 339

TYPE: PAT

ORGANISM: Homo sepiens
                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: XL, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Publication No.
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Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas
Carter, Darrick
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Hepler, William T.
                          Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
                                                                                            Day, Craig H.
Vedvick, Thomas
Carter, Darrick
                                                                                                                                                                          Jiang, Yuqiu
Kalos, Michael D.
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Vinals de Bassols, Carlota
Hural, John
                                                                                                                                           Retter, Marc W.
Stolk, John A.
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               Henderson,
                                                                                                                                                                                                                                                                                        Application US/09895814
b. US20020193296A1
                                                                            i, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , Samuel X.
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                                                                                                           Thomas S
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 116; DB 9;
100.0%; Pred. No. 1.7e-10;
tive 0; Mismatches 0;
               Robert A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 339;
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           Sequence 2, Application US/10010667A
Publication No. US20030055217A1
GENERAL INFORMATION:
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APPLICANT: Afar, Daniel
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GENERAL INFORMATION:

APPLICANT: Afar, Banel

APPLICANT: Hubert, Rene S.

APPLICANT: Leong, Mahan

APPLICANT: Leong, Mahan

APPLICANT: Battano, Arthur B.

APPLICANT: Saffran, Douglas C.

APPLICANT: Mitchell, Steve Chappell

APPLICANT: Mitchell, Steve Chappell

APPLICANT: Mitchell, Steve Chappell

APPLICANT: MITCHELL, STEVE CHAPPLICATION INFORMER: US/10/011,095

CURRENT APPLICATION NUMBER: 09/123,873

PRIOR APPLICATION NUMBER: 09/23,873

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUMBER: 60/097,183

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR BILLING DATE: 1998-6-61

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR ELING DATE: 1998-6-61

PRIOR APPLICATION NUMBER: 60/091,183

PRIOR ELING DATE: 1986-651

PRIOR BILLING DATE: 1986-651
US-10-010-667A-2
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US-09-895-814-879
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SOFTMARE: PRECED for Windows Version 3.0
SEC ITHN 879
LENGTH: 339
TERSTH: 339
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Publication No. US20030045682A1
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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APPLICANT: POY, Teresa
TITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILL REFERENCE: 201011 42726
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT PILLING_DATE: 2001-06-29
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OTHER INFORMATION: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 REVIHPLATSHQQYFYKIPILV 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 100.0%; Score 116; DB 9;
Local Similarity 100.0%; Pred. No. 1.7e-10;
ses 22; Conservative 0; Mismatches 0;
                                                                                                                                                  1 REVIHPLATSHOOYFYKIPILV 22
                                                                                                                 REVIHPLATSHOOYFYKIPILV 113
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Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                   100.0%; Score 116; DB 9; 100.0%; Pred. No. 1.7e-10; O. Mismatches 0;
                                                                                                                                                                                                                                                                                        Length 339;
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Rene S.

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CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT PILING DARE: 200.-01-12
NUMBER OF SEQ ID NOS: 934
SOFTHARS: PASTSEQ for Windows Version 3.0
SEQ ID NOS: PASTSEQ FOR WINDOWS VERSION 3.0
SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ ID SEQ I
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APPLICANT: Saftran, Douglas C.

APPLICANT: Micchell, Seeve Chappell

APPLICANT: Micchell, Seeve Chappell

TITLE OF INVENTION. MOVEL SERBEBRITHE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION. EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: $11582001601

FULLE REFERENCE: $1052001601

FULLE REFERENCE: $1052001

FULL REFERENCE: $1052001

FULLE REFERENCE: $1052001

FULLE REFERENCE: $1052001

FULL REFERENCE: $1052001

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US-09-759-143-879
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LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Skeiky, Yasix A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
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Vedvick, Thomas S.
Carter, Darrick
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                                                                                               100.0%; Score 116; DB 10; 100.0%; Pred. No. 1.7e-10; tive 0; Mismatches 0;
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Pred. No. 1
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Sequence 879, Application US/09822827

Bettert N. USZOŻOZOBISCOAL

GENERAL IMPORMATION:
APPLICANT: X. JAUSCHIM
APPLICANT: X. JAUSCHIM
TITLE OF INVENTION COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LICANOSIS OF PROSTATE CANCER
TILLE BEFERNICTION INDICATOR SAND METHODS FOR THE THERAPY AND
TURBERT APPLICATION NUMBER: US/09/822,827
CURRENT APPLICATION DATE: 2001-03-28
1 NUMBER OF SEG ID NOS: 860-103-28
2 NUMBER OF SEG ID NOS: 861-03-28
3 NOPMARK OF SEG ID NOS: 861-03-28
3 NOPMARK PRECEDE FOR MINDOWS Version 3.0
3 SEC ID NO 879
3 LENGTH: 339
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US-09-780-669-879
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION WOMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: PASTEDQ FOR WINDOWS Version 3.0
LENGTH: 339
TYPE: PRT
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Best Local Similarity
Matches 22; Conserv
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Hepler, William
Hural, John
McNeill, Patricia D.
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Mitcham, Jennifer L.
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ick, Thomas S.
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4    /cgm2 e/prodate/1/iaa/6A_COMB.pep;
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6    /cgm2 e/prodate/1/iaa/backfleesi.pep;
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(c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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APPLICANT: Daniel E. Afar
APPLICANT: Rene S. Hubert
APPLICANT: Kane S. Hubert
APPLICANT: Arbhan Leong
APPLICANT: Arbhar B. Raitano
APPLICANT: Arbhar B. Raitano
APPLICANT: Steve Chappell Mitchell

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ALIGNMENTS

US-09-323-873A-19

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Sequence 19, Application US/09323873A

PATENT NO. 6329503

GENERAL INFORMATION:

APPLICANT: Maniel E. Afar

APPLICANT: Rene S. Habert

APPLICANT: Anthur B. Raitano

APPLICANT: Athur B. Raitano

APPLICANT: Steve Chappell Mitchell

APPLICANT: Steve Chappell Mitchell

APPLICANT: Steve Chappell Mitchell

TITLE OF INVENTION: NOVEL SERREBNINE TRANSMEMBANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: 129 16USIT: 1990-66-10

FILOR APPLICATION NUMBER: 60/087,520

PRIOR APPLICATION NUM
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CURRENT APPLICANTON NUMBER: US/09/323,873A
CURRENT ELIXIO DATE: 1999-06-01
PRIOR PELICATION NUMBER: 60/087,520
PRIOR PELICATION NUMBER: 60/087,520
PRIOR PELICATION NUMBER: 60/091,183
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PATENT NO. 6390370

RESURBAL INFORMATION:
APPLICANT; LYND DOISCELE-Stamm et al

TITLE OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCCUS

TITLE OF INVERTION: DEPIDEMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TILE REFERENCE: GTC-007

CURENT APPLICATION NUMBER: US/09/134,001C

CURENET APPLICATION NUMBER: US/09/134,001C

CURENET APPLICATION NUMBER: US/09/134,001C

PRICE REPORTION NUMBER: US/09/134,001C

PRICE REPORTION NUMBER: US/09/134,001C

PRICE REPORTION NUMBER: US/09/134,001C

PRICE REPORTION NUMBER: US/09/134,001C
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TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
FILE REFERENCE: 129.1605U2
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Staphylococcus epidermidis
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                                                                                                                                                  APPLICANT: ZAMB., TIM
APPLICANT: ETZPATRICK, DAVID
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE 1
TITLE OF INVENTION: POLYPEPTIDES AND VACCINES
NOMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 195
                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BABIUK, LORNE
APPLICANT: VAN DEN HURK, SYLVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 RSLLSPLKTSYQEWQYQI 145
STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 100.0%; Score 116; Local Similarity 100.0%; Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 REVIHPLATSHQQYFYKI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Conservative
PALO ALTO
                                      755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.7%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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APPLICANT: FALCO, S. CAR1

APPLICANT: FRANCU, LAYO O.

APPLICANT: OCCOCO, Buddy

APPLICANT: OCCOCO, Buddy

APPLICANT: OCCOCO, Buddy

APPLICANT: Schwaber, James S.

TITLE OF INVENTION: Plant Aninoacyl-trNA Synthetase

FILE REFERENCE: BB-1193

CURRENT ELING DATE: 1999-07-209

CURRENT FILING DATE: 1999-07-209

EARLIER RILING DATE: 1999-07-209

EARLIER NELING DATE: JULY 21, 1998

EARLIER TILING DATE: JULY 21, 1998

NIMBER OF SEQ ID NOS: 37

COMMUNICATION OFFICE OF
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                                                   Query Match
Best Local Similarity
7; Conserva
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                                                                                                                                             US-09-357-251-24
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                                                                                                                                                                                                 SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/09357251
Patent No. 6271441
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                        TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 933 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPTER READABLE FORM;
MEDIUM TYBE: Floppy disk
COMPTER: 1BM PC compatible
COMPTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660 RELVEPCTANHKRYF 674
55 HPARDSHDTFFLKAP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 494-0792
                              5 HPLATSHOOYFYKIP 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 REVIHPLATSHOOYF 15
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                                                                        Conservative
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                                                                                       36.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.9%; Score 44; DB
40.0%; Pred. No. 71;
Live 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/682,847
                                                                                       Score 42;
Pred. No.
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                                                                        Mismatches
                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                            Length 284;
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; Sequence 3888, Application US/09134001C ; Patent No. 6380370

US-09-134-001C-3888

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US-08-471-112A-4
                                                                                  COMPUTER: IEBM PC COMPANIED COMPUTER: OCHONIC STREET COMPANIES STREET, PC-DOS/MS-DOS
SOFTWARE: PC-TOS/MS-DOS
SOFTWARE: PARENTIN Elease #1.0, Version #1.30
CURRENT.APPLICATION DATA:
APPLICATION WINDER: US/08/471,112A
FILING DATE: 06-UNN-1995
CLASSIFICATION DATA: PSE-1995
FILING DATE: 13-PEB-1995
FILING DATE: 13-PEB-1995
FILING DATE: 13-PEB-1995
FILING DATE: 13-PEB-1995
FILING DATE: 05-SEP-1995
FILING DATE: 05-SEP-1995
FILING TAPPLICATION WINDER: US/08/207,975
FILING DATE: 06-WAR-1994
ATTORNEY/AGENT INCREEN: US/08/207,975
PRICH APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: NAME: SIEMMANI, MICHAEL T.
REGISTRATION WINDER: 07/26
REGISTRATION WINDER: 07/26
FILING DATE: 06-WAR-1994
ATTORNEY/AGENT INCREEN: 07/26
REGISTRATION WINDER: 07/26
REGISTRATION WINDER: 08/207,975
FRIENDER/CE/DOCKET NUMBER: 07/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08471112A
Patent No. 6313264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3888
LENGTH: 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Staphylococcus epidermidis -09-134-001C-3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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NITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
NITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EFFECTOR PROTEINS OF RAPAMYCIN NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 IHKYCSDHQQRFYNCSI 265
                                                                       TELECOMMUNICATION INFORMATION:
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Local Similarity 47.1%;
nes 8; Conservarium
TELEPHONE: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 IHPLATSHQQYFYKIPI 20
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Nakanishi, Koji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Failli, Amedeo F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molnar-Kimber, Katherine L.
                                                  202-408-4000
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Pred. No. 45;
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                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-012-515A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50...
""Thes 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12,
Patent No. 6
                                                            Matches
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                   TELEFAX: 617-832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARES PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: IMNUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chiu, Maria Isabel APPLICANT: Cottarel, Guillaume
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1809 amino acids
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Damagnez, Veronique TITLE OF INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: APTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Berlin,
943 RQLDHPLPTVHPQVTY 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: C. STREET: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 RQLDHPLPTVHPQVTY 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109-2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: FOLEY, HOAG & ELIOT LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                              NAME: Vincent, Matthew P
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 REVIHPLATSHOOYFY 16
                            1 REVIHPLATSHOOYFY 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1140 amino acids
                                                          Conservative
                                                                                                                                                                                                                                                   617-832-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.2%;
                                                                           36.2%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                             US 08/360,144
                                                                                                                                                                                                                                                                                                                                                                                                                     US/09/012,515A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
Pred. No.
                                                                           Score 42;
Pred. No. 3
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
1.8e+02;
                                                                           .1e+02;
                                                                                        Length 1809;
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                                                            <u>.</u>
                                                            Gaps
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                                                            0
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RESULT 9 US-08-360-144A-12

36.2%;

Score 42; Pred. No.

DB 4; 3.1e+02;

Length 1809;

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APPLICANT: Berlin, V.

APPLICANT: Chiu I.

APPLICANT: Chiu I.

APPLICANT: Conterel, G.

APPLICANT: Conterel, G.

APPLICANT: Conterel, V.

TITLE OF INTERVISIO: IMMINOSUPPRESSANT TARGET PROTEINS

FILE REPRENCE: APPL-095-036

CURRENT EPPLICATION NUMBER: US/09/012,504A

CURRENT FILING DATE: 1998-01-23

PRICOR APPLICATION NUMBER: 09/360,144

PRICOR APPLICATION NUMBER: 09/360,144

PRICOR FILING DATE: 1998-12-20

PRICOR PILING DATE: 1998-12-20
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US-09-012-504A-12
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                                                                                    SEQ ID NO 12
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                                                                                                   PRIOR APPLICATION NUMBER: 08/250,795
PRIOR FILING DATE: 1994-05-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                     ORGANISM: Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Deternin PC-1088 #1.0, Version #1.30
CURRENT LEPLICATION DATA:
                                                               ENGTH: 1809
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LENGTH: 1809 amino acids
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REGISTRATION NUMBER: 36 7.09
REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-632-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: COTTATE, GUILLAUME
PPLICANT: Damagnez, Veronique
FITLE OP INVENTION: IMMUNOSUPPRESSANT TARGET PROTEINS
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Local Similarity 50.0%;
hes 8; Conservative
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Pred. No. 3.1e+02;
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Best Local Similarity
"hes 8; Conserv
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                                                                   Matches
                                                                                               Query Match
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                                                                                                                                                                                                                                                      TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
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1683 RQLDHPLPTVHPQVTY 1698
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARES: PACENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                  TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 2549 amino aci
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 0:
FILING DATE: 26-SEP-1995
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-FEB-1995
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TITLE OF INVENTION: EFFECTOR PROTEINS OF RAPAMYCIN
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 08-MAR-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                 Local Similarity
                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,276
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CLASSIFICATION: 536
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                                1 REVIHPLATSHOOYFY 16
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                                                                   Mismatches
                                                                                   4.5e+02,
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US-08-581-148C-18
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                                                       COMPUTER READALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DS/NS-DOS

SOFTWARE: Patentin Release #1.0, Vers

CURRENT APPLICATION NDTA:

1. PPLICATION NUMBER: US/08/581,148C

FILING DATE: 9-DE-1995

FILING DATE: 9-DE-1995
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           ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
REGISTRATION NUMBER: 352
                                                                                                                                                                                                                                   STREET: 17-
STREET: 17-
CITY: Chicago
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MOLECULE TYPE: protein
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APPLICATION NUMBER: 1
FILING DATE: 20-DEC-
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OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Immunosuppressant Target Proteins NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Xia, Xiji
TITLE OF INVENTION: GENES
TITLE OF INVENTION: GENES
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nes 8; Conserv
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REFERENCE/DOCKET NUMBER: 71380
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amino acid
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50.0%; Pred. No.
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                                                                                                                               Version #1.30
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, MOLECULE TYPE: protein US-08-581-148C-18
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MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: DADBY/MS-DOS
OMPTHARE: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION NUMBER: US/08/759,436
FILING DATE: 5-Dec-1996
ATTORNEY/AGENT INFORMATION:
NAME: COTd, Janet 1.
NAME: COTd, Janet 1.
REGISTRATION NUMBER: 33,778
REGISTRATION NUMBER: 31,718
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Patent No. 6
GENERAL INF
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Best Local Similarity
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TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-708-1935
TELEPAK: 212-246-8959
INFORMATION FOR SEQ ID NO: 3:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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174 VIHPFA-EHIAYFILFAIPLL 193
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TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
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Local Similarity 52.4%;
nes 11; Conservative
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                       3 VIHPLATSHQQYF--YKIPIL 21
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                                                                                         35.8%; Score 41.5; DB 4; Length 625; 52.4%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fatty aldehyde decarbonylage activity, recombinant molecules comprising said fragment and a method for obtaining transformed bacterial cells and plants
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA fragment encoding a protein
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Pred. No. 1.1e+02;
                                                                         2
                                                                         Mismatches
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RESULT 15 US-08-759-436-5

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FILLING DATE: 5-bec 1996
ATTORNEY/AGENT INFORMATION:
NAME: COT4, Janet 1.
REGISTRATION NUMBER: 33,778
REGISTRATION WHEER: 33,778
REPERENCE/DOCKET NUMBER: U01163-5 '
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-708-1935
TELEPHONE: 212-708-1935
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS;
SEQUENCE CHARACTERISTICS;
SEGUENCE CHARACTERISTICS;
STRANDENNESS;
STRANDENNESS;
                                                                              Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                         PEATURE:
NAME/KEY: Protein
LOCATION: 1.625
PUBLICATION INFORMATION:
AUTHORS: Aarte, Mark G.M.
AUTHORS: Keljzer, Christian J.
AUTHORS: Keljzer, Christian J.
AUTHORS: Stlekems, Willen J.
AUTHORS: Poreira, Andy
TITLE: of Arabidopsis involved in epicuticular wax
TITLE: biesynthesis and pollen fertility
LOURNAL: Plant Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARED PACEPALT RE-Lease #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Arabidopsis thaliana
STRAIN: Columbia ecotype
DEVELOPHENTAL STRAES: light and dark grown seedlings;
DEVELOPHENTAL STRAES: rosette and whole plants
IMMEDIATE SOURCE;
LIBRARY: PRL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
174 VIHPFA-EHIAYFILFAIPLL 193
                                                                                                                                                                                                       PAGES: 2115-2127

DATE: december-1995

RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO
                                                                                                                                                                                                                                                                                                                      JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 26 West 61st Street
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                                       3 VIHPLATSHOOYF--YKIPIL 21
                                                                                        35.8%; Score 41.5; DB 4; Length 6 ilarity 52.4%; Pred. No. 1.1e+02; Conservative 2; Mismatches 5; Indels
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                                                                                                                                         Length 625;
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Search completed: March 26, 2003, 16:51:39 Job time : 16.0698 secs